

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 08:57:16 ; Search time 16.833 Seconds
(without alignments)
1277.688 Million cell updates/sec

Title: US-10-718-321-6_COPY_40_81

Perfect score: 225

Sequence: 1 PLYSYTDCGNTVTSSDGL.....NNQTQFLFLESLTANTTKG 42

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	225	100.0	359	2	O43656 homo sapien
2	225	100.0	364	2	Q96D42
3	178	79.1	451	2	Q95144
4	178	79.1	460	2	O18984 cercopithec
5	178	79.1	469	2	O71448 cercopithec
6	178	79.1	473	2	O71447 cercopithec
7	178	79.1	474	2	O46597 cercopithec
8	178	79.1	478	2	O46598
9	62.5	27.8	639	1	YHR7 YEAST
10	62	27.6	842	2	Q9U0J9
11	61.5	27.3	1269	2	O97Z06
12	61	27.1	1255	2	O36287
13	60.5	26.9	3056	2	Q7USQ0
14	60	26.7	602	1	NRG1 CHICK
15	59	26.2	142	2	O6KPY4
16	59	26.2	549	2	O53969
17	59	26.2	559	2	O36298
18	59	26.2	626	2	O6KHE7
19	59	26.2	1254	1	POLS_EWVE
20	59	26.2	1254	2	Q77VY8
21	59	26.2	1259	2	Q9YKCS
22	59	26.2	2951	2	O8THC9
23	58.5	26.0	931	2	Q6WP59
24	58.5	26.0	931	2	Q6WP60
25	58.5	26.0	931	2	Q6WP63
26	58.5	26.0	931	2	Q6WP68
27	58.5	26.0	931	2	Q6WP69
28	58.5	26.0	931	2	Q6WP70
29	58.5	26.0	1258	2	Q9WC27
30	58.5	26.0	3392	2	Q8JQD9
31	58.5	26.0	3392	2	Q91NH1

32	58.5	26.0	3392	2	Q6WP58	Q6wp58 dengue viru
33	58.5	26.0	3392	2	Q80KC7	Q80kc7 dengue viru
34	58	25.8	558	2	O36293	O36293 venezuelan
35	58	25.8	558	2	O36294	O36294 venezuelan
36	58	25.8	559	2	O36297	O36297 venezuelan
37	58	25.8	559	2	O36308	O36308 venezuelan
38	58	25.8	559	2	O36309	O36309 venezuelan
39	58	25.8	559	2	O41997	O41997 venezuelan
40	58	25.8	559	2	Q8V5J7	Q8v5j7 venezuelan
41	58	25.8	559	2	Q8V5J8	Q8v5j8 venezuelan
42	58	25.8	559	2	Q98755	Q98755 venezuelan
43	58	25.8	559	2	Q9WCF9	Q9wcf9 venezuelan
44	58	25.8	559	2	Q9WCG0	Q9wcg0 venezuelan
45	58	25.8	1254	1	POLS_REVW8	P05674 venezuelan

ALIGNMENTS

RESULT 1						
O43656						
ID	O43656	PRELIMINARY;	PRT;	359 AA.		
AC	O43656;					
DT	01-JUN-1998 (TREMBLrel. 06, Created)					
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)					
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)					
DE	Hepatitis A virus cellular receptor 1.					
GN	Name=HAVcr-1;					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=Liver;					
RX	MEDLINE=98325180; PubMed=9658108;					
RA	Feigelstock D., Thompson P., Mattoo P., Zhang Y., Kaplan G.G.;					
RT	"The human homolog of HAVcr-1 codes for a hepatitis A virus cellular receptor."					
RL	J. Virol. 72:6621-6628(1998).					
DR	EMBL; AF043724; AAC39862.1; -.					
DR	GO; GO:0004872; F:receptor activity; IEA.					
DR	InterPro; IPR003599; IG.					
DR	InterPro; IPR007110; IG-like.					
DR	SMART; SM00409; IG; 1.					
DR	PROSITE; PS50835; IG LIKE; 1.					
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.					
KW	Receptor.					
SQ	SEQUENCE 359 AA; 38704 MW; C207FEC562DC62CA CRC64;					
Query Match	100.0%;	Score 225;	DB 2;	Length 359;		
Best Local Similarity	100.0%;	Pred. No. 2.8e-20;	Mismatches 0;	Indels 0;	Gaps 0;	
Matches 42;	Conservative 0;					
Qy	1 PLYSYTDCGNTVTSSDGLMNNQTLFLESLTANTTKG 42					
Db	249 PLYSYTDCGNTVTSSDGLMNNQTLFLESLTANTTKG 290					
RESULT 2						
Q96D42						
ID	Q96D42	PRELIMINARY;	PRT;	364 AA.		
AC	Q96D42;					
DT	01-DEC-2001 (TREMBLrel. 19, Created)					
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)					
DT	25-OCT-2004 (TREMBLrel. 28, Last annotation update)					
DE	HAVCR1 protein.					
GN	Name=HAVCR1;					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
OX	NCBI_TaxID=9606;					

RN SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RC SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RP Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC013325; AAH13325.1; --
 DR EMBL; CR457114; CAG33395.1; --
 DR Genew; HGNC:17866; HAVCR1.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR SMART; SM00409; IG_1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 SQ SEQUENCE 364 AA; 39249 MW; AA67C7DC7FAC81F1 CRC64;
 Query Match 100.0%; Score 225; DB 2; Length 364;
 Best Local Similarity 100.0%; Pred. No. 2.8e-20; Mismatches 0; Indels 0; Gaps 0;
 Matches 42; Conservative 0;
 QY 1 PLYSYTGDNDVTVESSDGLWNNNTQLFLEHSLTANTTKG 42
 Db PLYSYTGDNDVTVESSDGLWNNNTQLFLEHSLTANTTKG 295
 RESULT 3
 QY5144 PRELIMINARY; PRT; 451 AA.
 AC QY5144;
 DT 01-FEB-1997 (TRENBLrel. 02, Created)
 DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
 DE HAVCR-1 protein precursor.
 OS Cercopithecus aethiops (Green monkey) (Grivet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=9534;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=97015129; PubMed=8861957;
 RA Kaplan G., Totsuka A., Thompson P., Akatsuka T., Moritsugu Y.,
 RA Feinstein S.M.;
 RT "Identification of a surface glycoprotein on African green monkey

RT kidney cells as a receptor for hepatitis A virus.";
 RL EMBL; J. 15:4282-4296(1996).
 DR PIR; S71754; S71754.1; --
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR SMART; SM00409; IG_1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Signal.
 FT SIGNAL 1 17 Potential.
 SQ SEQUENCE 451 AA; 48774 MW; 5D395C5455AA4332 CRC64;
 Query Match 79.1%; Score 178; DB 2; Length 451;
 Best Local Similarity 81.0%; Pred. No. 3.6e-14; Mismatches 2; Indels 0; Gaps 0;
 Matches 34; Conservative 2;
 QY 1 PLYSYTGDNDVTVESSDGLWNNNTQLFLEHSLTANTTKG 42
 Db PLYSYTGDNDVTVESSDGLWNNNTQLFLEHSLTANTTKG 370
 RESULT 4
 OI8984 PRELIMINARY; PRT; 460 AA.
 AC OI8984;
 DT 01-JAN-1998 (TRENBLrel. 05, Created)
 DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Hepatitis A virus receptor.
 OS Cercopithecus aethiops (Green monkey) (Grivet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=9534;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97368416; PubMed=9225030;
 RA Ashida M., Hamada C.;
 RT "Molecular cloning of the hepatitis A virus receptor from a simian
 RT cell line.";
 RL J. Gen. Virol. 78:1565-1569(1997).
 DR EMBL; D88585; BAA21556.1; --
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR SMART; SM00409; IG_1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Receptor.
 SQ SEQUENCE 460 AA; 49687 MW; 1D1A0C1D832139EA CRC64;
 Query Match 79.1%; Score 178; DB 2; Length 460;
 Best Local Similarity 81.0%; Pred. No. 3.7e-14; Mismatches 2; Indels 0; Gaps 0;
 Matches 34; Conservative 2;
 QY 1 PLYSYTGDNDVTVESSDGLWNNNTQLFLEHSLTANTTKG 42
 Db PLYSYTGDNDVTVESSDGLWNNNTQLFLEHSLTANTTKG 379
 RESULT 5
 QYJ48 PRELIMINARY; PRT; 469 AA.
 AC QYJ48;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DE Hepatitis A virus cellular receptor 1 short form.
 GN Name=HAVCr-1;
 OS Cercopithecus aethiops (Green monkey) (Grivet).

OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC	Cercopitheciinae; Cercopithecus.
ON	NCBI_TaxID=9534;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=98285791; PubMed=9621093;
RA	Feigelsstock D., Thompson P., Mattoo P., Kaplan G.G.;
RT	"Polymorphisms of the hepatitis A virus cellular receptor 1 in African
RT	green monkey kidney cells result in antigenic variants that do not
RT	react with protective monoclonal antibody 190/4.";
RL	J. Virol. 72:6218-6222(1998).
DR	ENBL; AF043446; AAC39771.1; -.
DR	GO; GO:0004872; F:receptor activity; IEA.
DR	InterPro; IPR003599; Ig.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003006; Ig_MHC.
DR	SMART; SM00409; IG; 1.
DR	PROSITE; PS00835; IG LIKE; 1.
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW	Receptor.
SQ	SEQUENCE 469 AA; 50561 MW; 27E386F47948F528 CRC64;
Query Match 79.1%; Score 178; DB 2; Length 469;	
Best Local Similarity 81.0%; Pred. No. 3.7e-14;	
Matches 34; Conservative 2; Mismatches 6; Indels 0; Gaps 0;	
QY	1 PLSYTTDGDNDVTVESSDGLWNNTQLFLHSLLTANTTKG 42
DB	347 PLSYTTDGDNDVTVESSDGLWNNTQLSPHSQMWNTTEG 388
RESULT 6	
Q7JJ47	PRELIMINARY; PRT; 473 AA.
ID	Q7JJ47
AC	Q7JJ47; 2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Hepatitis A virus cellular receptor 1 short form.
GN	Name=HAVcr-1;
OS	Cercopithecus aethiops (Green monkey) (Grivet).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC	Cercopitheciinae; Cercopithecus.
ON	NCBI_TaxID=9534;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=98285791; PubMed=9621093;
RA	Feigelsstock D., Thompson P., Mattoo P., Kaplan G.G.;
RT	"Polymorphisms of the hepatitis A virus cellular receptor 1 in African
RT	green monkey kidney cells result in antigenic variants that do not
RT	react with protective monoclonal antibody 190/4.";
RL	J. Virol. 72:6218-6222(1998).
DR	ENBL; AF043448; AAC39773.1; -.
DR	GO; GO:0004872; F:receptor activity; IEA.
DR	InterPro; IPR003599; Ig.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003006; Ig_MHC.
DR	SMART; SM00409; IG; 1.
DR	PROSITE; PS00835; IG LIKE; 1.
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW	Receptor.
SQ	SEQUENCE 473 AA; 50973 MW; CD15EF5BE79C8013 CRC64;
Query Match 79.1%; Score 178; DB 2; Length 473;	
Best Local Similarity 81.0%; Pred. No. 3.8e-14;	
Matches 34; Conservative 2; Mismatches 6; Indels 0; Gaps 0;	
QY	1 PLSYTTDGDNDVTVESSDGLWNNTQLFLHSLLTANTTKG 42
DB	351 PLSYTTDGDNDVTVESSDGLWNNTQLSPHSQMWNTTEG 392


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OC Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=21332296; PubMed=11427726; DOI=10.1073/pnas.141222098;
RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Awayez M.J., Chan-Welher C.C.-Y., Clausen I.G., Curtis B.A.,
RA De Moors A., Brauso G., Fletcher C., Gordon P.M.K.,
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840 (2001).
DR EMBL; AF006730; AAK41392.1; -.
DR PIR; A90267; A90267.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001611; LRR.
DR PRINTS; PR00019; LEURICRPT_
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Complete proteome; Protease.
SQ SEQUENCE 1269 AA; 138027 MW; 87C8F05CCF83DA84 CRC64;

Query Match 27.3%; Score 61.5; DB 2; Length 1269;
Best Local Similarity 34.0%; Pred. No. 85;
Matches 18; Conservative 7; Mismatches 11; Indels 17; Gaps 2;

OY 4 SYTDG-----NDVTVE-SSDGLMNNQTLFLESLTANT 39
DB 1163 SPTTNGTHIVTINTQNPYDGYNLVTATIQDGLSSSSSYLYFENGTLNLT 1215

RESULT 12
O36287 PRELIMINARY; PRT; 1255 AA.
AC O36287; O36301;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Structural polyprotein.
OS Venezuelan equine encephalitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
OC Alphavirus; VEEV complex.
OX NCBI_TaxID=11036;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=66637, and 66457;
RX MEDLINE=97404681; PubMed=9261393;
RA Powers A.M., Oberste M.S., Brault A.C., Rico-Hesse R., Schmura S.M.,
RA Smith J.F., Kang W., Sweeney W.P., Weaver S.C.;
RT "Repeated emergence of epidemic/epizootic Venezuelan equine
RT encephalitis from a single genotype of enzootic subtype ID virus.";
RL J. Virol. 71:6697-6705 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=66637, and 66457;
RX MEDLINE=99214366; PubMed=10196323;
RA Wang E., Barrera R., Boshell J., Ferro C., Freier J.E., Navarro J.C.,
RA Salas R., Vasquez C., Weaver S.C.;
RT "Genetic and phenotypic changes accompanying the emergence of
RT epizootic subtype IC Venezuelan equine encephalitis viruses from an
RT enzootic subtype ID progenitor.";
RL J. Virol. 73:4266-4271 (1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=66637, and 66457;
RA Wang E., Weaver S.C.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF004458; AAC71187.2; -.

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DR EMBL; AF004472; AAC71997.2; -.
DR HSSP; P05674; 1EPS.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002548; Alpha_E1_glycop.
DR InterPro; IPR000936; Alpha_E2_glycop.
DR InterPro; IPR002533; Alpha_E3_glycop.
DR InterPro; IPR000336; Flavi_glycoprote.
DR InterPro; IPR000930; Peptidase_S3.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00944; Alpha_core; 1.
DR Pfam; PF01589; Alpha_E1_glycop; 1.
DR Pfam; PF00943; Alpha_E2_glycop; 1.
DR Pfam; PF01563; Alpha_E3_glycop; 1.
DR PRINTS; PR00798; TOGAVIRIN.
KW Polyprotein.
SQ SEQUENCE 1255 AA; 138339 MW; 799350E33C807EAA CRC64;

Query Match 27.1%; Score 61; DB 2; Length 1255;
Best Local Similarity 47.6%; Pred. No. 97;
Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 11 DTVTESSDGLMNNQTLFLE 31
DB 758 ETIWESLDHLNNNQMFWIQ 778

RESULT 13
O7USQ0 PRELIMINARY; PRT; 3056 AA.
ID O7USQ0;
AC O7USQ0;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Probable extracellular nuclease.
OS OrderedLocusNames=RB4375;
OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
DR EMBL; BX294140; CAD73746.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0007154; P:cell communication; IEA.
DR InterPro; IPR006034; Asp/Glutamase.
DR InterPro; IPR003644; Calx_beta.
DR InterPro; IPR003368; Chlamydia_PMP.
DR InterPro; IPR002105; Dockerin_1.
DR InterPro; IPR006626; Pbh1.
DR InterPro; IPR011050; Pectin_lyas_like.
DR InterPro; IPR011506; Planc_extracel.
DR Pfam; PF03160; Calx-beta; 1.
DR Pfam; PF02415; Chlam_PMP; 59.
DR Pfam; PF00404; Dockerin_1; 2.
DR Pfam; PF07595; Planc_extracel; 1.
DR SMART; SM00710; Pbh1; 32.
DR PROSITE; PS00144; ASN_GLN_ASE_1; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 3056 AA; 296490 MW; A305EF2F431BF67 CRC64;

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Query Match          26.9%; Score 60.5; DB 2; Length 3056;
Best Local Similarity 31.1%; Pred. No. 3.1e+02;
Matches 14; Conservative 6; Mismatches 14; Indels 11; Gaps 2;

QY 8 DGN-----DVTSSGGLMNNNTQTFLFSLHSLTANTTKG 42
   ||| : ||||| : : : ||| :
Db 306 DGNADISGTTIRDTNFAREGGLMNNNTGT-MIVDGTILTGNVASG 349

RESULT 14
NRGL_CHICK
ID NRGL_CHICK STANDARD; PRT; 602 AA.
AC Q05199; O73750; O73751; O73752;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pro-neuregulin-1 precursor (Pro-NRGL) [Contains: Neuregulin-1
DE (Acetylcholine receptor inducing activity) (ARIA)].
GN Name=NRGL1; Synonyms=ARIA;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.
RC STRAIN=White leghorn; TISSUE=Brain;
RX MEDLINE=93203602; PubMed=8453670; DOI=10.1016/0092-8674(93)90407-H;
RA Falls D.L., Rosen K.M., Corfas G., Lane W.S., Fischbach G.D.;
RT "ARIA, a protein that stimulates acetylcholine receptor synthesis, is
RT a member of the neu ligand family.";
RL Cell 72:801-815 (1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 2; 3 AND 4).
RC TISSUE=Brain, and Spinal cord;
RX MEDLINE=98150951; PubMed=9491987; DOI=10.1016/S0896-6273(00)80454-7;
RA Yang X., Kuo Y., Devay P., Yu C., Role L.;
RT "A cysteine-rich isoform of neuregulin controls the level of
RT expression of neuronal nicotinic receptor channels during
RT synaptogenesis.";
RL Neuron 20:255-270 (1998).
CC -!- FUNCTION: Direct ligand for the ERBB tyrosine kinase receptors.
CC The multiple isoforms perform diverse functions: cysteine-rich
CC domain containing isoforms (isoforms 2-4) probably regulate the
CC expression of nicotinic acetylcholine receptors at developing
CC interneuronal synapses. The Ig-NRG isoform is required for the
CC initial induction and/or maintenance of the mature levels of
CC acetylcholine receptors. The Ig-NRG isoform exists as a type I membrane
CC protein.
CC -!- SUBCELLULAR LOCATION: Exists as a type I membrane protein and as a
CC proteolytically released soluble growth factor form. The membrane-
CC bound form does not seem to be active (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Comment=Additional isoforms seem to exist;
CC Name=1; Synonyms=ARIA, IG-NRG;
CC IsoId=Q05199-1; Sequence=Displayed;
CC Note=Contains an Ig-like domain;
CC Name=2; Synonyms=CRD-NRG-BETA1;
CC IsoId=Q05199-2; Sequence=VSP_003445;
CC Note=The EGF-like domain is replaced by a cysteine-rich domain
CC (CRD);
CC Name=3; Synonyms=CRD-NRG-BETA2A;
CC IsoId=Q05199-3; Sequence=VSP_003445, VSP_003446;
CC Note=The EGF-like domain is replaced by a cysteine-rich domain
CC (CRD);
CC Name=4; Synonyms=CRD-NRG-BETA2B;
CC IsoId=Q05199-4; Sequence=VSP_003445, VSP_003446, VSP_003447,
CC VSP_003448;
CC Note=The EGF-like domain is replaced by a cysteine-rich domain
CC (CRD);
CC -!- DEVELOPMENTAL STAGE: Isoforms 2-4 are detected at embryonic day 4
CC (ED4) in both visceral and somatic motor neurons of spinal cord
CC and is highest at ED6. Isoform 1 is not expressed until ED 6 in

```

```

spinal cord. At ED 11 both isoforms display comparable levels.
-!- DOMAIN: The cytoplasmic domain may be involved in the regulation
of trafficking and proteolytic processing. Regulation of the
proteolytic processing involves initial intracellular domain
dimerization (By similarity).
-!- DOMAIN: ERBB receptor binding is elicited entirely by the EGF-like
domain.
-!- PTM: Proteolytic cleavage close to the plasma membrane on the
external face leads to the release of the soluble growth factor
form.
-!- PTM: Extensive glycosylation precedes the proteolytic cleavage (By
similarity).
-!- SIMILARITY: Belongs to the neuregulin family.
-!- SIMILARITY: Contains 1 EGF-like domain.
-!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
-----
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or send an email to license@isb-sib.ch).
-----
EMBL; L11264; AAA49037.1; -.
DR EMBL; AF045654; AAC05670.1; -.
DR EMBL; AF045655; AAC05671.1; -.
DR EMBL; AF045656; AAC05672.1; -.
DR F1R; A45769; A45769.
DR HSSP; Q12780; 1HRE.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR002154; Neuregulin.
DR Pfam; PF00047; Ig 1.
DR Pfam; PF02158; Neuregulin; 1.
DR PRINTS; PR01089; NEUREGULIN.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; FALSE_NEG.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS00835; IG_Like; 1.
KW Alternative splicing; Direct protein sequencing; EGF-like domain;
KW Glycoprotein; Growth factor; Immunoglobulin domain; Transmembrane.
FT CHAIN 1 602
FT CHAIN 1 205
FT DOMAIN 1 206 Extracellular (Potential).
FT TRANSMEM 207 229 Internal signal sequence (Potential).
FT DOMAIN 230 602 Cytoplasmic (Potential).
FT DOMAIN 29 123 Ig-like C2-type.
FT DOMAIN 125 136 Ser/Thr-rich.
FT DOMAIN 137 181 EGF-like.
FT DISULFID 49 105 By similarity.
FT DISULFID 141 155 By similarity.
FT DISULFID 149 169 By similarity.
FT DISULFID 171 180 By similarity.
FT CARBOHYD 21 21 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 113 113 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 126 126 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 1 127
MMATSEGLQYSLAPTQDQVNSVNTVPKLEKMNQEVAV
CQKLVRCETTSSEPALAFKWLKXGKEITKKNRPENKIPK
KQKYSEUHIITRATLADAGEYACRVSSKLGNDSTKASVIIT
DTNA -> MSVVGTEFTFPPSAQLSPDASLGLPAENMPG
PHREDSRVPGVAGLAKTCCVCLAEARLXGCLNSEKICIAPI
LACLLSLCLCTAGLKWFDKIFEDYDPTHLDPGRIGQDPR
STVDPTALSAVPSVEVAPFPPIPSLESKAEVTVOTDSLV
PSRPPLQPSLXNRILVGLWSSAPFSLSPLEPTASQAO
ARETNLQTPAKUS (in isoform 2, isoform 3
and isoform 4).
/FTId=VSP_003445.

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Search completed: June 29, 2005, 09:01:43
Job time : 17.833 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 29, 2005, 09:46:27 ; Search time 25.4145 Seconds
(without alignments)
635.503 Million cell updates/sec

Title: US-10-718-321-6_COPY_40_81

Perfect score: 225

Sequence: 1 PLYSYTDGNDVTVESSDGL.....NNQTLFLEHLLTANTTKG 42

Scoring table: BLASTUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 487488

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*
1: /cgm2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgm2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgm2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgm2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgm2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgm2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgm2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgm2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgm2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgm2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgm2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgm2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgm2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgm2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgm2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgm2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgm2_6/ptodata/1/pubpaa/US10F_PUBCOMB.pep.*
19: /cgm2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgm2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgm2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgm2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	99	44.0	18	17	US-10-718-321-1
2	48	21.3	44	15	US-10-424-599-190016
3	48	21.3	48	15	US-10-424-599-282496
4	47.5	21.1	40	15	US-10-424-599-264613
5	46	20.4	44	15	US-10-424-599-240616
6	45	20.0	49	15	US-10-424-599-179504
7	43.5	19.3	31	15	US-10-424-599-284397
8	43.5	19.3	42	16	US-10-437-963-166786
9	43	19.1	43	9	US-09-925-300-1031
10	42.5	18.9	43	16	US-10-425-115-191318
11	42	18.7	35	15	US-10-424-599-216152

12	42	18.7	42	15	US-10-424-599-265756	Sequence 265756,
13	42	18.7	42	15	US-10-424-599-277738	Sequence 277738,
14	42	18.7	50	16	US-10-425-115-367358	Sequence 367358,
15	41.5	18.4	37	15	US-10-424-599-269343	Sequence 269343,
16	41	18.2	32	16	US-10-425-115-328576	Sequence 328576,
17	41	18.2	37	16	US-10-425-115-330334	Sequence 330334,
18	41	18.2	39	16	US-10-425-115-194419	Sequence 194419,
19	41	18.2	39	16	US-10-608-029-29	Sequence 29, Appl
20	40.5	18.0	34	16	US-10-425-115-333901	Sequence 333901,
21	40.5	18.0	36	15	US-10-424-599-264025	Sequence 264025,
22	40	17.8	14	14	US-10-193-477-75	Sequence 75, Appl
23	40	17.8	33	15	US-10-432-412-16	Sequence 16, Appl
24	40	17.8	40	16	US-10-425-115-186134	Sequence 186134,
25	40	17.8	42	9	US-09-185-908-6	Sequence 6, Appl
26	40	17.8	42	10	US-09-482-682-25	Sequence 25, Appl
27	40	17.8	49	10	US-09-824-438-9	Sequence 9, Appl
28	39.5	17.6	25	16	US-10-601-656-56	Sequence 56, Appl
29	39.5	17.6	25	17	US-10-873-015-69	Sequence 69, Appl
30	39.5	17.6	42	17	US-10-472-928-730	Sequence 730, App
31	39	17.3	30	16	US-10-716-029-275	Sequence 275, App
32	39	17.3	30	16	US-10-425-115-362870	Sequence 362870,
33	39	17.3	43	15	US-10-424-599-147295	Sequence 147295,
34	39	17.3	46	15	US-10-424-599-203943	Sequence 203943,
35	39	17.3	46	16	US-10-425-115-200490	Sequence 200490,
36	39	17.3	47	16	US-10-425-115-232897	Sequence 232897,
37	39	17.3	47	16	US-10-425-115-362227	Sequence 362227,
38	39	17.3	48	15	US-10-424-599-179725	Sequence 179725,
39	39	17.3	49	15	US-10-424-599-147420	Sequence 147420,
40	39	17.3	49	16	US-10-425-115-222102	Sequence 222102,
41	38.5	17.1	48	15	US-10-305-133-18	Sequence 18, Appl
42	38.5	17.1	49	16	US-10-425-115-324897	Sequence 324897,
43	38	16.9	28	14	US-10-121-799-2	Sequence 2, Appl
44	38	16.9	28	14	US-10-404-626-2	Sequence 2, Appl
45	38	16.9	28	20	US-11-033-209-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-10-718-321-1
; Sequence 1, Application US/10718321
; Publication No. US20050112117A1
; GENERAL INFORMATION:
; APPLICANT: Biogen Idec Ma Inc.
; APPLICANT: Bailey, Veronique
; APPLICANT: Bonventre, Joseph
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: Molecules and Methods for Inhibiting
; FILE OF INVENTION: Shedding of KIM-1
; FILE REFERENCE: A124 US
; CURRENT APPLICATION NUMBER: US/10/718,321
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/295449
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/295907
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US02/17402
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-718-321-1

Query Match 44.0%; Score 99; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 SSDGLNNNQTLFLEHS 33
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Db 1 SSDGLWNNNQTLFLEHS 18

RESULT 2
US-10-424-599-190016
; Sequence 190016, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 190016
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_142603C.1.pep
US-10-424-599-190016

Query Match 21.3%; Score 48; DB 15; Length 44;
Best Local Similarity 37.9%; Pred. No. 54;
Matches 11; Conservative 7; Mismatches 7; Indels 4; Gaps 1;

QY 12 TWTSSDGLWNNN----QTQLFLEHSLLT 36
||| ||| :||| :||| :||| :|||
| ||| :||| :||| :||| :|||
Db 2 TPTQSSLFYHSNTSLSTSPFIKSLTT 30

RESULT 3
US-10-424-599-282496
; Sequence 282496, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 282496
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_97115C.1.pep
US-10-424-599-282496

Query Match 21.3%; Score 48; DB 15; Length 48;
Best Local Similarity 39.3%; Pred. No. 59;
Matches 11; Conservative 3; Mismatches 8; Indels 8; Gaps 1;

QY 20 LWNNNQTLFLEHSLTA-----NTTK 41
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Db 7 MWKNRQTKSFLERHVLPGMSQHYRNLTK 34

RESULT 4
US-10-424-599-264613
; Sequence 264613, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
```

```
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 264613
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_80967C.1.pep
US-10-424-599-264613

Query Match 21.1%; Score 47.5; DB 15; Length 40;
Best Local Similarity 40.0%; Pred. No. 56;
Matches 12; Conservative 3; Mismatches 10; Indels 5; Gaps 1;

QY 11 DTVTSSDGLWNNNQTLFLEHSLLTATT 40
: ||| ||| : ||| : ||| : |||
| ||| : ||| : ||| : |||
Db 7 EHTELDSPLMQNNLFI-----LTATTS 31

RESULT 5
US-10-424-599-240616
; Sequence 240616, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 240616
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_59303C.1.pep
US-10-424-599-240616

Query Match 20.4%; Score 46; DB 15; Length 44;
Best Local Similarity 36.8%; Pred. No. 1e+02;
Matches 14; Conservative 5; Mismatches 9; Indels 10; Gaps 3;

QY 1 PLYSYTTDGNDTVTSSDGLWNNNQTLFLEHSLTAN 38
||| : ||| : ||| : |||
Db 11 PLFIY-----YKSSSES-WNSKNKNLF-SHDAHTFN 38

RESULT 6
US-10-424-599-179504
; Sequence 179504, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
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; SEQ ID NO 179504
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_133108C.1.pep
US-10-424-599-179504

Query Match      20.0%; Score 45; DB 15; Length 49;
Best Local Similarity 29.4%; Pred. No. 1.6e+02;
Matches 10; Conservative 8; Mismatches 14; Indels 2; Gaps 1;

QY 10 NDTVTSSDGLWNNQTQLFL--EHSLLTANTTK 41
Db 2  SDNAKSSADSYNDRSDVYLIDYEHNLVSSNTEK 35

RESULT 7
US-10-424-599-284397
; Sequence 284397, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 284397
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_98836C.1.pep
US-10-424-599-284397

Query Match      19.3%; Score 43.5; DB 15; Length 31;
Best Local Similarity 37.5%; Pred. No. 1.4e+02;
Matches 9; Conservative 7; Mismatches 5; Indels 3; Gaps 1;

QY 21 WNNNTQTLFLEHSLTANTTK 41
Db 5  WNSRTYLVQFILENQLLSLSASK 28

RESULT 8
US-10-437-963-166786
; Sequence 166786, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 166786
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_65460C.1.pep
US-10-437-963-166786

Query Match      19.3%; Score 43.5; DB 16; Length 42;
Best Local Similarity 47.8%; Pred. No. 2.1e+02;
Matches 11; Conservative 6; Mismatches 3; Indels 3; Gaps 2;

QY 20 LMNNNTQTLF-LEHSLTANTTK 41
Db 15 IWTLNTTKLYLLKHTLL--NSTK 35

RESULT 9
US-09-925-300-1031
; Sequence 1031, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1031
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1031

Query Match      19.1%; Score 43; DB 9; Length 43;
Best Local Similarity 40.9%; Pred. No. 2.5e+02;
Matches 9; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 21 WNNNTQTLFLEHSLTANTTK 42
Db 21 WDYRHEQLHLVHMLLIVEEVKG 42

RESULT 10
US-10-425-115-191318
; Sequence 191318, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 191318
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_106061C.1.pep
US-10-425-115-191318

Query Match      18.9%; Score 42.5; DB 16; Length 43;
Best Local Similarity 29.0%; Pred. No. 2.9e+02;
```



```
Matches 9; Conservative 6; Mismatches 11; Indels 5; Gaps 1;
QY 1 PLYSYTTDGNVTYESSDG-----LWNNQQT 26
|: : |::| |::| |::|
Db 6 PMIFFAGDAHDTCVETPGGRSIRWPNSSST 36
|: : |::| |::| |::|
RESULT 11
US-10-424-599-216152
; Sequence 216152, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 216152
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_37214C.1.pap
US-10-424-599-216152
Query Match 18.7%; Score 42; DB 15; Length 35;
Best Local Similarity 56.2%; Pred. No. 2.7e+02;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 PLYSYTTDGNVTYTES 16
|: : |::| |::| |::|
Db 12 PERSYTTGSLTKTKS 27
|: : |::| |::| |::|
RESULT 12
US-10-424-599-265756
; Sequence 265756, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 265756
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_81999C.1.pap
US-10-424-599-265756
Query Match 18.7%; Score 42; DB 15; Length 42;
Best Local Similarity 47.1%; Pred. No. 3.3e+02;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 17 SDGLWNNQQTQFLFLEHS 33
|: : |::| |::| |::|
Db 17 STTLWNNWDFIFIEHN 33
|: : |::| |::| |::|
RESULT 13
US-10-424-599-277738
```

```
; Sequence 277738, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 277738
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_92820C.1.pap
US-10-424-599-277738
Query Match 18.7%; Score 42; DB 15; Length 47;
Best Local Similarity 34.2%; Pred. No. 3.8e+02;
Matches 13; Conservative 6; Mismatches 11; Indels 8; Gaps 2;
QY 3 YSYTTDGNVTYTE-SSDGLWNNQQTQFLFLEHSLTLTANT 39
|: : |::| |::| |::| |::|
Db 7 YTYHTANMDAVVDVSLSDVTDNNKTS-----YTANT 37
|: : |::| |::| |::| |::|
RESULT 14
US-10-425-115-367358
; Sequence 367358, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 367358
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_98200C.1.pap
US-10-425-115-367358
Query Match 18.7%; Score 42; DB 16; Length 50;
Best Local Similarity 42.9%; Pred. No. 4.1e+02;
Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
QY 20 LWNNQQTQFLFLEHS 33
|: : |::| |::| |::|
Db 9 VMSNHRVRGFLQHS 22
|: : |::| |::| |::|
RESULT 15
US-10-424-599-269343
; Sequence 269343, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
```

```
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 269343
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_85237C.1.pep
US-10-424-599-269343
```

```
Query Match      18.4%; Score 41.5; DB 15; Length 37;
Best Local Similarity 37.5%; Pred. No. 3.3e+02;
Matches 12; Conservative 3; Mismatches 16; Indels 1; Gaps 1;
```

```
OY      1 PLYSYTTDGNQDTVTSSDGLMNNQTLPLEH 32
      ||| | | | | | | | | | | | | | |
Db      4 PLYRVTLSVSSDD-CKHLDLISNKQTHYSLRH 34
```

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Search completed: June 29, 2005, 10:14:19
Job time : 26.4145 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 29, 2005, 09:03:05 ; Search time 28.7151 Seconds
(without alignments)
565.693 Million cell updates/sec

Title: US-10-718-321-6_COPY_40_81
Perfect score: 225
Sequence: 1 PLYSTTGNDVFTSSDGL.....NNQTQLFLEHLLTANTTKG 42

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 938430

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_16Dec04:*
- 1: Geneseqp19808:*
 - 2: Geneseqp19908:*
 - 3: Geneseqp20008:*
 - 4: Geneseqp20018:*
 - 5: Geneseqp20028:*
 - 6: Geneseqp20038:*
 - 7: Geneseqp20038s:*
 - 8: Geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	44.9	18	6	Aao26686 Human KIM
2	99	44.0	18	6	Aao26687 Human KIM
3	99	44.0	18	6	Aao26673 Monoclonal
4	90	40.0	18	6	Aao26688 Human KIM
5	82	36.4	18	6	Aao26685 Human KIM
6	48.5	21.6	40	8	Ad807403 Staphyloc
7	46	20.4	49	4	Aam92081 Human dig
8	45.5	20.2	40	2	Aaw25651 Rat cadhe
9	45.5	20.2	40	2	Aaw13116 Rat cadhe
10	44.5	19.8	31	2	Aar85818 Peptide r
11	44	19.6	20	2	Aaw08045 HIV pepri
12	43	19.1	43	3	Ad56453 Human pro
13	42.5	18.9	20	8	Ad195222 OSPF-rela
14	42	18.7	40	2	Aar43565 Rat cadhe
15	42	18.7	40	2	Aaw25648 Rat cadhe
16	42	18.7	40	2	Aaw13113 Rat cadhe
17	42	18.7	49	2	Aar83059 Human IL-
18	41.5	18.4	32	2	Aaw18789 Z peptide
19	41	18.2	46	4	Aam24315 Rat Est e
20	41	18.2	46	7	Adf60572 Human con
21	41	18.2	46	1	Adf59574 Human pol
22	41	18.2	49	7	AdP59574 Modified
23	41	18.2	50	5	Abp11026 Human ORF
24	40.5	18.0	50	4	Abg30194 Novel hum
25	40	17.8	14	7	Ade03490 BGS-3 aep

ALIGNMENTS

RESULT 1
AAO26686

ID AAO26686 standard; peptide; 18 AA.

XX AAO26686;

AC AAO26686;

DT 20-MAR-2003 (first entry)

XX Human KIM-1 mucin domain related peptide, SEQ ID No 14.

XX Cytostatic; gene therapy; antibody; antigen; antigen-binding;

KW proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;

XX renal disease; injury; renal cancer.

OS Synthetic.

XX WO200298920-A1.

XX 12-DEC-2002.

XX 31-MAY-2002; 2002WO-US017402.

XX 01-JUN-2001; 2001US-0295449P.

XX 04-JUN-2001; 2001US-0295907P.

(BIOJ) BIOGEN INC.

(GEO) GEN HOSPITAL CORP.

PI Bailly V, Bonventre J;

XX WPI; 2003-156845/15.

XX New antibody, antibody derivative or antigen-binding polypeptide that

inhibits proteolytic release of a soluble kidney injury molecule-1

polypeptide, useful for treating or preventing renal disease or injury,

XX Disclosure; Fig 1A; 42pp; English.

XX The invention relates to a novel antibody, antibody derivative or antigen

-binding polypeptide that inhibits proteolytic release of a soluble

kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.

XX The antibody, antibody derivative or antigen-binding polypeptide is

Ado10179 Human int
Aae28518 Neisseria
Aab34080 Human sec
Adf48735 Adenovira
Aar84975 Peptide r
Abu00797 S. pneumo
Aaw35650 Rat cadhe
Aaw13115 Rat cadhe
Aab20698 Polymeric
Aar85528 Sugar con
Aab34079 Human sec
Aag50726 Arabinops
Aar5014 Peptide r
Aar85810 Peptide r
Ada22738 Therapeut
Aay34178 Human pre
Aap70718 Equine in
Ade36036 Anaplasma
Ade72984 E. equi m
Aaw62593 Peptide h

```
SQ Sequence 18 AA;
  Query Match          44.9%; Score 101; DB 6; Length 18;
  Best Local Similarity 100.0%; Pred. No. 5.3e-06;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 7 TDGNDTVTSSDGLWNNN 24
  DB 1 TDGNDTVTSSDGLWNNN 18
  RESULT 2
  ID AAO26687
  AC AAO26687 standard; peptide; 18 AA.
  XX
  XX
  DT 20-MAR-2003 (first entry)
  DE Human KIM-1 mucin domain related peptide, SEQ ID No 15.
  XX
  XX Cytostatic; gene therapy; antibody; antigen; antigen-binding;
  KW proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;
  KW renal disease; injury; renal cancer.
  XX
  XX Synthetic.
  OS
  XX WO200298920-A1.
  PN
  XX
  PD 12-DEC-2002.
  XX
  XX
  PF 31-MAY-2002; 2002WO-US017402.
  XX
  XX Human KIM-1 mucin domain related peptide, SEQ ID No 15.
  DE
  XX Cytostatic; gene therapy; antibody; antigen; antigen-binding;
  KW proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;
  KW renal disease; injury; renal cancer.
  XX
  XX Synthetic.
  OS
  XX WO200298920-A1.
  PN
  XX
  PD 12-DEC-2002.
  XX
  PF 31-MAY-2002; 2002WO-US017402.
  XX
  XX 01-JUN-2001; 2001US-0295449P.
  PR
  PR 04-JUN-2001; 2001US-0295907P.
  XX
  XX (BIOJ ) BIOGEN INC.
  PA (GEO ) GEN HOSPITAL CORP.
  XX
  XX Bailly V, Bonventre J;
  PI
  XX WPI; 2003-156845/15.
  DR
  XX
  PT New antibody, antibody derivative or antigen-binding polypeptide that
  PT inhibits proteolytic release of a soluble kidney injury molecule-1
  PT polypeptide, useful for treating or preventing renal disease or injury,
  PT e.g. renal cancer.
  XX
  PS Claim 4; Page 25; 42pp; English.
  XX
  CC The invention relates to a novel antibody, antibody derivative or antigen
  CC -binding polypeptide that inhibits proteolytic release of a soluble
  CC kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.
  CC The antibody, antibody derivative or antigen-binding polypeptide is
  CC useful for treating or preventing renal disease or injury, e.g. renal
  CC cancer. The antibody is also useful for inhibiting shedding of the KIM-1
  CC polypeptide. This sequence represents a binding epitope of the invention
  SQ Sequence 18 AA;
  Query Match          44.0%; Score 99; DB 6; Length 18;
  Best Local Similarity 100.0%; Pred. No. 9.6e-06;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 16 SSDGLWNNNTQLFLEHS 33
  DB 1 SSDGLWNNNTQLFLEHS 18
  RESULT 4
  ID AAO26688
  AC AAO26688 standard; peptide; 18 AA.
  XX
  XX AAO26688;
  XX
  DT 20-MAR-2003 (first entry)
  DE Human KIM-1 mucin domain related peptide, SEQ ID No 16.
  XX
  XX Cytostatic; gene therapy; antibody; antigen; antigen-binding;
  KW proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;
  KW renal disease; injury; renal cancer.
  XX
  XX Synthetic.
  OS
  XX WO200298920-A1.
  PN
  XX
```

```
SQ Sequence 18 AA;
  Query Match          44.0%; Score 99; DB 6; Length 18;
  Best Local Similarity 100.0%; Pred. No. 9.6e-06;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 16 SSDGLWNNNTQLFLEHS 33
  DB 1 SSDGLWNNNTQLFLEHS 18
  RESULT 3
  ID AAO26673
  AC AAO26673 standard; peptide; 18 AA.
  XX
```



```
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0251990P.
PR 05-JAN-2001; 2001US-0254097P.
PR 05-JAN-2001; 2001US-0254097P.
PA (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-502630/55.
DR N-PSDB; AAK87854.
XX Polynucleotides encoding digestive system antigens, useful for
PT diagnosing, treating, preventing and/or prognosing disorders of the
PT digestive system, particularly cancer and cancer metastases.
XX Claim 11; SEQ ID NO 1430; 986pp; English.
PS The present invention provides the protein and coding sequences of a
XX number of human digestive system antigens. These can be used in the
CC diagnosis, treatment and prevention of digestive system disorders,
CC including cancer, Meckel's diverticulum, bacterial or parasitic
CC infections, appendicitis, Hirschsprung's disease, chronic colitis or
CC ulcerative colitis. The present sequence is a digestive system antigen of
CC the invention
XX
XX Query Match 20.4%; Score 46; DB 4; Length 49;
XX Best Local Similarity 33.3%; Pred. No. 2.3e+02;
XX Matches 9; Conservative 3; Mismatches 15; Indels 0; Gaps 0;
XX
XX 2 LYSYTTGNDVTWESSDGLWNNNQTL 28
QY

DB 23 IMKYSTQGDQKXEGKASLWNLHTML 49
RESULT 8
AAW25651
ID AAW25651 standard; protein; 40 AA.
XX
AC AAW25651;
XX
DT 25-MAR-2003 (revised)
DT 04-NOV-1997 (first entry)
XX
DE Rat cadherin-10 cytoplasmic domain.
XX
KW Human; cadherin; rat; calcium-dependent cell adhesion protein;
KW superfamily; cytoskeleton; eatenin; cancer.
XX
OS Rattus rattus.
XX
PN US5646250-A.
XX
PD 08-JUL-1997.
XX
PF 01-NOV-1994; 94US-00332638.
XX
PR 17-APR-1992; 92US-00872643.
PR 19-APR-1993; 93US-00049460.
XX
PA (DOHE-) DOHENY EYE INST.
XX
PI Suzuki S;
XX
WPI; 1997-362997/33.
DR N-PSDB; AAT85426.
XX
PT Human and rat cadherin polypeptide(s) - mediate cell-cell adhesion.
XX
PS Example 1; Col 29-30; 56pp; English.
XX
CC This sequence represents the cytoplasmic domain of rat cadherin-10. The
CC invention specifically provides details of human cadherin-5, -8, -11, -12
CC and -13, and rat cadherin-8, -5, -11 and -13. Cadherins are calcium-
CC dependent cell adhesion proteins. They are glycosylated integral membrane
CC proteins that have an N-terminal extracellular domain that determines
CC binding specificity, a hydrophobic membrane spanning region and a C-
CC terminal cytoplasmic domain, which is highly conserved among members of
CC the superfamily. The C-terminal domain interacts with the cytoskeleton
CC through eatenins and other cytoskeleton-associated proteins. The novel
CC cadherin proteins may be used in the analysis of the role of cadherins in
CC various cancers. Sequence analysis of the cadherin proteins also allows
CC investigation of the structure and function of cadherin. The cadherin
CC proteins may be isolated by using anti-cadherin antibodies. These
CC antibodies may also be used to modulate the activity of cadherin and to
CC determine the tissue specific distribution of cadherin proteins. Each
CC subclass of cadherins has a unique tissue distribution pattern. (Updated
CC on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 40 AA;
XX
XX Query Match 20.2%; Score 45.5; DB 2; Length 40;
XX Best Local Similarity 31.7%; Pred. No. 2.1e+02;
XX Matches 13; Conservative 5; Mismatches 8; Indels 15; Gaps 1;
XX
QY 2 LYSYTTGNDVTWESSDGLWNNNQTLFLEHSLTANTTKG 42
DB 2 LATIAYEGNDSVAESL-----SSLESGETEG 27
XX
RESULT 9
AAW13116
ID AAW13116 standard; protein; 40 AA.
XX
```


DR WPI; 1996-432980/43.

XX Determining the likelihood of maternal transmission of HIV-1 to foetus -

PT by measuring maternal reactivity with specific gp120 and gp41 derived

PT peptide(s), also used for diagnosing HIV in infants.

XX

PS Disclosure; Col 59-60; 63pp; English.

XX

CC AAW08016-W08073 represent HIV peptides that can be used in the method of

CC the invention. The method of the invention is for determining whether or

CC not a mother will transmit HIV-1 to a foetus. The method comprises

CC incubating a sample from the HIV-infected mother, with a collection of

CC HIV peptides. The HIV peptides includes at least one gp41 derived peptide

CC (see AAW07918-W07928), and at least one HIV gp120 derived peptide (see

CC AAW07909-W07917). The number of peptides that react with the sample is

CC determined, and this number is compared with a standard that shows

CC pattern reactivity for a patient of transmission status. A non-

CC transmissible HIV sample is indicated if the test sample reacts with twice

CC as many peptides as the standard. The method detects the presence of

CC neutralising antibodies that protect against mother to infant

CC transmission of HIV. These sequences can also be used in vaccines to

CC protect against transmission. Antibodies against these sequences can be

CC used for passive immunisation, and to generate anti-idiotypic antibodies

CC for use in vaccines or active immunotherapy. (Updated on 16-OCT-2003 to

CC standardise OS field)

XX

SQ Sequence 20 AA;

Query Match 19.6%; Score 44; DB 2; Length 20;

Best Local Similarity 39.1%; Pred. No. 1.4e+02;

Matches 9; Conservative 4; Mismatches 2; Indels 8; Gaps 1;

QY 1 PLYSYTTDGNVTSSDGLWNN 23

Db ||:|:|:|

2 PLFNSTWNGNNT-----WNN 16

RESULT 12

AAB56453

ID AAB56453 standard; protein; 43 AA.

XX

AC AAB56453;

XX

DT 13-MAR-2001 (first entry)

XX

DE Human prostate cancer antigen protein sequence SEQ ID NO:1031.

XX

KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;

KW neuroprotective; cytostatic; cardioprotective; immunomodulatory; muscular;

KW vulnary; gastrointestinal; nephrotropic; antiinfective; gynaecological;

KW antibacterial; gene therapy; neural; immune; reproductive; renal;

KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;

KW wound; infectious disease.

XX

OS Homo sapiens.

XX

PN WO200055174-A1.

XX

PD 21-SEP-2000.

XX

PF 08-MAR-2000; 2000WO-US005988.

XX

PR 12-MAR-1999; 99US-0124270P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

PA (ROSE/) ROSEN C A.

XX

PI Rosen CA, Ruben SM;

XX

DR WPI; 2000-587513/55.

DR N-PSDB; AAF15656.

XX

PT Prostate cancer associated gene sequences, referred to as prostate cancer

antigens, useful for treatment, prevention, and diagnosis of disorders

such as prostate cancer.

Claim 11; Page 1460; 2338pp; English.

AAF15566 to AAF16505 encode the human prostate cancer associated

proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.

The prostate cancer antigens can have neuroprotective, cytostatic,

cardioactive, immunomodulatory, muscular, vulnary, gastrointestinal,

nephrotropic, antiinfective, gynaecological and antibacterial activities,

and can be used in gene therapy. The prostate cancer antigen

polynucleotides may be used for detection of prostate cancer, chromosome

identification, as chromosome markers, and for numerous other diagnostic

or research purposes. The prostate cancer antigens may be used to treat

disorders such as neural, immune, muscular, reproductive,

gastrointestinal, pulmonary, cardiovascular, renal, and proliferative

disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to

AAB57303 represent sequences used in the exemplification of the present

invention

Sequence 43 AA;

Query Match 19.1%; Score 43; DB 3; Length 43;

Best Local Similarity 40.9%; Pred. No. 4.7e+02;

Matches 9; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 21 WNNNTQLEHSLTANTTKG 42

Db ||:|:|:|

21 WDYRHEQLHVMLLIVEVKG 42

RESULT 13

ADI95222

ID ADI95222 standard; peptide; 20 AA.

XX

AC ADI95222;

XX

DT 04-NOV-2004 (first entry)

XX

DE OSPF-related SIV envelope (Env) peptide - SEQ ID 130.

XX

KW immune response; overlapping synthetic peptide formulation; OSPF;

KW immunostimulant; virucide; antibacterial; antiparasitic; cytostatic;

KW vaccine; viral; bacterial; parasitic infection; prion disease;

KW neoplastic; toxin; SIV; envelope; Env.

XX

OS Simian immunodeficiency virus.

XX

PN WO2004002415-A2.

XX

PD 08-JAN-2004.

XX

PF 27-JUN-2003; 2003WO-US020322.

XX

PR 27-JUN-2002; 2002US-0392718P.

XX

PA (DAND) DANA FARBER CANCER INST INC.

XX

PI Ruprecht RM, Jiang S;

XX

DR WPI; 2004-082868/08.

XX

PT Modulating an immune response, useful for treating immune disorders, e.g.

PT viral, bacterial and parasitic infections, prion diseases, or neoplastic

PT diseases, administering to a subject an overlapping synthetic peptide

PT formulation.

XX

PS Example 1; SEQ ID NO 130; 175pp; English.

XX

CC The invention relates to a novel method for modulating an immune response

CC comprising administering to a subject an overlapping synthetic peptide

CC formulation (OSPF) which comprises a combination of single chain peptides

CC corresponding to the amino acid sequence of a protein of interest. The

```
CC method of the invention has immunostimulant, virucide, antibacterial,
CC antiparasitic and cytostatic applications and may be useful during
CC vaccine production and for treating immune disorders including viral,
CC bacterial and parasitic infections, prion diseases, neoplastic diseases,
CC as well as providing protection against toxins. The current sequence is
CC that of the OSPF-related SIV envelope (Env) peptide of the invention.
XX
XX
SQ Sequence 20 AA;
Query Match 18.9%; Score 42.5; DB 8; Length 20;
Best Local Similarity 52.6%; Pred. No. 2.1e+02;
Matches 10; Conservative 2; Mismatches 6; Indels 1; Gaps 1;
QY 13 VTSSDGLWNNQTLFLR 31
Db 1 VTSEFDA-WNNVTVEQAE 18
RESULT 14
AAR43565
ID AAR43565 standard; protein; 40 AA.
XX
AC AAR43565;
XX
DT 25-MAR-2003 (revised)
DT 19-JUN-1994 (first entry)
XX
DE Rat cadherin-7.
XX
KW Antibodies; binding.
XX
OS Rattus rattus.
XX
PN WO9321302-A1.
XX
PD 28-OCT-1993.
XX
PF 19-APR-1993; 93WO-US003681.
XX
PR 17-APR-1992; 92US-00872643.
XX
PA (DOHE-) DOHENY EYE INST.
XX
PI Suzuki S;
XX
WPI; 1993-351714/44.
DR N-PSDB; AAQ51223.
XX
DNA encoding cadherins (CH)6,7,9 and 10 antibodies to CH 5,6,7,9 and 10 -
XX useful for modulating binding and regulatory activities of cadherins.
PS Claim 14; Page 41; 99pp; English.
XX
Rat cadherins-7 was isolated from a rat brain and retina cDNA library
XX using degenerate PCR primers designed from highly conserved segments in
CC the cytoplasmic domain of mouse N-, E- and P cadherins. See also AAR43564
CC -7. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 40 AA;
Query Match 18.7%; Score 42; DB 2; Length 40;
Best Local Similarity 39.1%; Pred. No. 5.8e+02;
Matches 9; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
QY 2 LYSYTTDGNITVTSSDGLWNNN 24
Db 2 LQTYAFEGNGSVAESLSLSDSNS 24
RESULT 15
AAR25648
ID AAR25648 standard; protein; 40 AA.
XX
```

```
AC AAW25648;
XX
DT 25-MAR-2003 (revised)
DT 04-NOV-1997 (first entry)
XX
DE Rat cadherin-7 cytoplasmic domain.
XX
KW Human; cadherin; rat; calcium-dependent cell adhesion protein;
KW superfamily; cytoskeleton; eatenin; cancer.
XX
OS Rattus rattus.
XX
FH Key Location/Qualifiers
FT Misc-difference 40
FT /note= "Encoded by CTC"
XX
PN US5646250-A.
XX
PD 08-JUL-1997.
XX
PF 01-NOV-1994; 94US-00332638.
XX
PR 17-APR-1992; 92US-00872643.
PR 19-APR-1993; 93US-00049460.
XX
PA (DOHE-) DOHENY EYE INST.
XX
PI Suzuki S;
XX
WPI; 1997-362997/33.
DR N-PSDB; AAT85423.
XX
Human and rat cadherin polypeptide(s) - mediate cell-cell adhesion.
XX
Example 1; Col 27-28; 56pp; English.
XX
This sequence represents the cytoplasmic domain of rat cadherin-7. The
XX invention specifically provides details of human cadherin-5, -8, -11, -12
XX and -13, and rat cadherin-8, -5, -11 and -13. Cadherins are calcium-
XX dependent cell adhesion proteins. They are glycosylated integral membrane
XX proteins that have an N-terminal extracellular domain that determines
XX binding specificity, a hydrophobic membrane spanning region and a C-
XX terminal cytoplasmic domain, which is highly conserved among members of
XX the superfamily. The C-terminal domain interacts with the cytoskeleton
XX through eatenins and other cytoskeleton-associated proteins. The novel
XX cadherin proteins may be used in the analysis of the role of cadherins in
XX various cancers. Sequence analysis of the cadherin proteins also allows
XX investigation of the structure and function of cadherin. The cadherin
XX proteins may be isolated by using anti-cadherin antibodies. These
XX antibodies may also be used to modulate the activity of cadherin and to
XX determine the tissue specific distribution of cadherin proteins. Each
XX subclass of cadherins has a unique tissue distribution pattern. (Updated
XX on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 40 AA;
Query Match 18.7%; Score 42; DB 2; Length 40;
Best Local Similarity 39.1%; Pred. No. 5.8e+02;
Matches 9; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
QY 2 LYSYTTDGNITVTSSDGLWNNN 24
Db 2 LQTYAFEGNGSVAESLSLSDSNS 24
Search completed: June 29, 2005, 09:41:05
Job time : 31.7151 secs
```

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	43.5	19.3	49	2	S49365	Ig mu chain transmembrane
2	42.5	18.9	46	2	A49281	pol protein - simi
3	39	17.3	30	2	D82251	hypothetical protein
4	38	16.9	35	2	S30112	aminoglycoside N6'
5	37	16.4	34	2	S69880	ribulose-bisphosphat
6	37	16.4	47	2	AF0464	hypothetical protein
7	37	16.4	48	2	S29150	superoxide dismuta
8	36.5	16.2	46	2	F49281	pol,protein - simi
9	36	16.0	50	2	D49410	t-complex polypept
10	35.5	15.8	29	2	A32860	biotin-binding pro
11	35.5	15.8	37	2	AG0540	hypothetical prote
12	35	15.6	50	2	A61149	endo-1,4-beta-xyla
13	34.5	15.3	46	2	D49281	pol protein - simi
14	34	15.1	31	2	S49191	hypothetical prote
15	34	15.1	40	2	PQ0202	endo-1,4-beta-xyla
16	34	15.1	41	2	F82525	hypothetical prote
17	33.5	14.9	40	2	H95183	hypothetical prote
18	33	14.7	38	2	S72344	pilB protein - Nei
19	32.5	14.4	31	2	H82682	hypothetical prote
20	32.5	14.4	46	2	E49281	pol protein - simi
21	32.5	14.4	48	2	PL0090	Ig heavy chain v r
22	32	14.2	24	2	A36912	hypothetical prote
23	32	14.2	26	2	B53113	Lys-gingipain form
24	32	14.2	28	2	G32351	34K class B flagel
25	32	14.2	29	2	I50214	protein-tyrosine-p
26	32	14.2	31	2	A57001	endo-1,4-beta-xyla
27	32	14.2	41	2	S56120	collagenase type I
28	32	14.2	42	2	I37543	MHC HLA-DR-beta-1
29	32	14.2	45	2	D45731	gene 39.2 protein

```
RESULT 3
D82251
hypotheical protein VC1030 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: D82251
R:Heidelbergl, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chardon, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: D82251
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-30 <HEI>
A:Cross-references: UNIPROT:Q9KT75; GB:AE004184; GB:AE003852; NID:99655483; PIDN:AAF9418
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC1030
A:Map position: 1

Query Match 17.3%; Score 39; DB 2; Length 30;
Best Local Similarity 61.5%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 28 LPLEHSLTANTT 40
DB 12 LFYEHELLRLNVT 24

RESULT 4
S30112
aminoglycoside N6'-acetyltransferase (EC 2.3.1.82) - Klebsiella pneumoniae plasmid pCF60
C:Species: Klebsiella pneumoniae
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-May-2000
C:Accession: S30112
R:Mabilat, C.; Lourencao-Vital, J.; Goussard, S.; Courvalin, P.
Mol. Gen. Genet. 235, 113-121, 1992
A:Title: A new example of physical linkage between Tn1 and Tn21: the antibiotic multiple
A:Reference number: S30112; MUID:93062798; PMID:1331747
A:Accession: S30112
A:Molecule type: DNA
A:Residues: 1-35 <NAB>
A:Cross-references: EMBL:X64525
C:Genetics:
A:Gene: aacA4
A:Genome: plasmid
C:Keywords: acyltransferase; antibiotic resistance; coenzyme A

Query Match 16.9%; Score 38; DB 2; Length 35;
Best Local Similarity 58.3%; Pred. No. 2.7e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 YSYTTDGNDDT 14
DB 24 YSIVTNSDSDVT 35

RESULT 5
S68880
ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain - kidney bean chloroplast (f
C:Species: Chloroplast Phaseolus vulgaris (kidney bean)
C>Date: 04-Dec-1997 #sequence_revision 04-Dec-1997 #text_change 09-Jul-2004
C:Accession: S68880
R:Yoshida, T.; Minamikawa, T.
Eur. J. Biochem. 238, 317-324, 1996
A:Title: Successive amino-terminal proteolysis of the large subunit of ribulose 1,5-bisph
A:Reference number: S68880; MUID:96283823; PMID:8681940
A:Accession: S68880
A:Molecule type: protein
A:Residues: 1-34 <YOS>
A:Cross-references: UNIPROT:Q7M2E2
```

```
C:Genetics:
A:Genome: chloroplast
A:Function:
A:Description: catalyzes the reaction of carbon dioxide with D-ribulose 1,5-bisphosphate
C:Superfamily: ribulose-bisphosphate carboxylase large chain
C:Keywords: Calvin cycle; carbon dioxide fixation; carbon-carbon lyase; carboxy-lyase; c

Query Match 16.4%; Score 37; DB 2; Length 34;
Best Local Similarity 47.1%; Pred. No. 3.5e+02;
Matches 8; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 5 YTTDGNDDVTTESSDGLW 21
DB 11 YTPDYETKDAESSIGTW 27

RESULT 6
AF0464
hypotheical protein YPO3815 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AF0464
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, I.
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AF0464
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-47 <KUR>
A:Cross-references: UNIPROT:Q8ZAI7; GB:AL590842; PIDN:CAC93282.1; PID:gl5981729; GSPDB:G
C:Genetics:
A:Gene: YPO3815

Query Match 16.4%; Score 37; DB 2; Length 47;
Best Local Similarity 39.1%; Pred. No. 5.1e+02;
Matches 9; Conservative 5; Mismatches 7; Indels 2; Gaps 1;

QY 17 SDGLWNNNTQTLFLEHSLTANT 39
DB 8 NNSLGYNNNVQVY--HFLDSNT 28

RESULT 7
S29150
superoxide dismutase (EC 1.15.1.1) (Cu-Zn) III, cytosolic - rice (fragment)
C:Species: Oryza sativa (rice)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: S29150; E61531
R:Kanematsu, S.; Asada, K.
Plant Cell Physiol. 31, 99-112, 1990
A:Title: Characteristic amino acid sequences of chloroplast and cytosol isozymes of CuZn-
A:Reference number: S29146
A:Accession: S29150
A:Molecule type: protein
A:Residues: 1-48 <KAN>
A:Cross-references: UNIPROT:Q7M237
R:Kanematsu, S.; Asada, K.
Free Radic. Res. Commun. 12, 383-390, 1991
A:Title: Chloroplast and cytosol isozymes of CuZn-superoxide dismutase: their characteris
A:Accession: E61531
A:Molecule type: protein
A:Residues: 1-48 <KA2>
C:Function:
A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C:Superfamily: superoxide dismutase [Cu-Zn]
C:Keywords: copper; cytosol; metalloprotein; oxidoreductase; zinc
F:44,46/Binding site: copper (His) #status predicted

Query Match 16.4%; Score 37; DB 2; Length 48;
```

RESULT 10

A32860
biotin-binding protein I - chicken (fragment)
C/Species: Gallus gallus (chicken)
C/Date: 22-Nov-1999 #sequence_revision 22-Nov-1989 #text_change 24-Jun-1993
C/Accession: A32860
R/Bush, L.; White III, H.B.
J. Biol. Chem. 264, 5741-5745, 1989
A/Title: Conversion of domains into subunits in the processing of egg yolk biotin-binding
A/Reference number: A32860; MUID:89174628; PMID:2925632
A/Accession: A32860
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-29 <BUS>

Query Match 15.8%; Score 35.5; DB 2; Length 29;
Best Local Similarity 52.9%; Pred. No. 4.5e+02;
Matches 9; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

QY 19 GLWNNQTQLFLEHSL 35
||| ||| ||| : |||
Db 9 GLWNEQDSL-MEISAL 24

RESULT 11

AG0540
hypothetical protein STY0342 [imported] - Salmonella enterica subsp. enterica serovar Typhi
C/Species: Salmonella enterica subsp. enterica serovar Typhi
A/Note: this species has also been called Salmonella typhi
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C/Accession: AG0540
R/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar
A/Reference number: AB0502; MUID:21534947; PMID:11677608
A/Accession: AG0540
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-37 <PAR>
A/Cross-references: GB:AL513382; PIDN:CAD08767.1; PID:gi16501585; GSPDB:GN00176
C/Genetics:
A/Gene: STY0342

Query Match 15.8%; Score 35.5; DB 2; Length 37;
Best Local Similarity 61.5%; Pred. No. 6e+02;
Matches 8; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 7 TDGNDTVTESSDG 19
||| ||| |||
Db 4 TDGNDN-TRKQDG 15

RESULT 12

A61149
endo-1,4-beta-xylanase (EC 3.2.1.8) - fungus (Trichoderma viride) (fragment)
C/Species: Trichoderma viride
C/Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
C/Accession: A61149
R/Ujije, M.; Roy, C.; Yaguchi, M.
Appl. Environ. Microbiol. 57, 1860-1862, 1991
A/Title: Low-molecular-weight xylanase from Trichoderma viride.
A/Reference number: A61149; MUID:91336731; PMID:1872616
A/Accession: A61149
A/Molecule type: protein
A/Residues: 1-50 <UJI>
A/Cross-references: UNIPROT:Q7MAV8
C/Function:
A/Description: catalyzes the hydrolysis of 1,4-beta-xylosidic linkages in xylans
A/Pathway: xylan degradation
C/Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

C;Keywords: glycosidase; hydrolase; polysaccharide degradation; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 15.6%; Score 35; DB 2; Length 50;
Best Local Similarity 58.3%; Pred. No. 9.8e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 YSYTTDGNQDVT 14
||| ||| :||
Db 15 YSYWNDHGGVT 26

RESULT 13

D49281

pol protein - simian T-cell lymphotropic virus type 1, STLV-1 (isolate Pat24) (fragment)
C;Species: simian T-cell lymphotropic virus type 1, STLV-1

C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004

C;Accession: D49281

R;Sakena, N.K.; Herve, V.; Durand, J.P.; Leguenno, B.; Diop, O.M.; Digoutte, J.P.; Math
; Paul, B.; Dube, D.K.; Barre-Sinoussi, F.; Poiesz, B.J.

Virology 198, 297-310, 1994

A;Title: Seroepidemiologic, molecular, and phylogenetic analyses of simian T-cell leukem
A;Reference number: A49281; PMID:8259665

A;Accession: D49281

A;Status: preliminary; translation not shown

A;Molecule type: DNA

A;Residues: 1-46 <SAK>

A;Cross-references: UNIPROT:Q88403; GB:L20353; NID:9431711; PIDN:AAA16557.1; PID:9431712

C;Superfamily: pol polyprotein

Query Match 15.3%; Score 34.5; DB 2; Length 46;
Best Local Similarity 36.4%; Pred. No. 1e+03;
Matches 12; Conservative 3; Mismatches 15; Indels 3; Gaps 2;

QY 2 LYSYTTDGNQDVTES--SDGLMNNNQTLFLEH 32
||| ||| :||| :||
Db 13 LYKYFTDKPDLPMDNALSTLTINHLNV-LTH 44

RESULT 14

S49191

hypothetical protein 6 - Azotobacter vinelandii (fragment)

C;Species: Azotobacter vinelandii

C;Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004

C;Accession: S49191

R;Wientjens, R.; van Dongen, W.; Haaker, H.

submitted to the EMBL Data Library, April 1992

A;Description: Molecular cloning of fixA, fixB, fixC and fixX genes of Azotobacter vinel
A;Reference number: S49186

A;Accession: S49191

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-31 <WIE>

A;Cross-references: UNIPROT:Q44509; EMBL:X65515

Query Match 15.1%; Score 34; DB 2; Length 31;
Best Local Similarity 54.5%; Pred. No. 7.5e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 24 NQTQLFLEHSL 34
||| ||| :||
Db 2 NDIQLFLAHAI 12

RESULT 15

PQ0202

endo-1,4-beta-xylanase (EC 3.2.1.8) II - Nocardiopsis dassonvillei (fragment)

C;Alternate names: xylanase

C;Species: Nocardiopsis dassonvillei

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004

C;Accession: PQ0202

R;Tsujibo, H.; Sakamoto, T.; Miyamoto, K.; Hasegawa, T.; Fujimoto, M.; Inamori, Y.

Agric. Biol. Chem. 55, 2173-2174, 1991

A;Title: Amino acid compositions and partial sequences of xylanases from a new subspecies
A;Reference number: PQ0202; PMID:92118324; PMID:1368735

A;Accession: PQ0202

A;Molecule type: protein

A;Residues: 1-40 <TSU>

A;Cross-references: UNIPROT:Q9R5P8

C;Experimental source: subsp. alba OPC-18

C;Comment: This enzyme is important for the breakdown of xylan.

C;Function:

A;Description: catalyzes the hydrolysis of 1,4-beta-xylosidic linkages in xylans

A;Pathway: xylan degradation

C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 15.1%; Score 34; DB 2; Length 40;
Best Local Similarity 50.0%; Pred. No. 1e+03;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 YSYTTDGNQDVT 14
||| ||| :||
Db 16 YSFWDGGGSVS 27

Search completed: June 29, 2005, 09:47:29

Job time : 6.611 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 09:03:05 ; Search time 55.3792 Seconds
(without alignments)
565.693 Million cell updates/sec

Title: US-10-718-321-6
Perfect score: 432
Sequence: 1 MFLPRQNHPEVATSPSSPOP.....NNQTQLFLEHLLTANTTKG 81

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 938430

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	23.4	18	6	AAO26686 Human KIM
2	99	22.9	18	6	AAO26687 Human KIM
3	99	22.9	18	6	AAO26673 Monoclonal
4	98	22.7	18	6	AAO26681 Human KIM
5	97	22.5	18	6	AAO26682 Human KIM
6	96	22.2	18	6	AAO26683 Human KIM
7	95	22.0	18	6	AAO26685 Human KIM
8	92	21.3	18	6	AAO26684 Human KIM
9	90	20.8	18	6	AAO26688 Human KIM
10	60	13.9	50	4	AAO20331 Peptide #
11	60	13.9	50	4	ABO40865 Peptide #
12	60	13.9	50	4	AAO34632 Peptide #
13	60	13.9	50	4	ABB25019 Protein #
14	60	13.9	50	4	AAO74520 Human bon
15	60	13.9	50	4	AAO61724 Human bra
16	60	13.9	50	4	ABG56310 Human liv
17	60	13.9	50	5	ABG44381 Human pep
18	54.5	12.6	40	6	ABR91655 P. papata
19	53	12.3	39	4	ABU53259 Human tes
20	52.5	12.2	47	3	AAO56300 Human sec
21	52	12.0	47	8	ABO59205 Human gen
22	51.5	11.9	50	4	ABO50592 Human sec
23	51.5	11.9	50	6	ABO44849 Novel hum
24	51.5	11.9	50	7	ABO26329 Protein a
25	50	11.6	35	4	AAO2139 Mouse alp

26	50	11.6	35	5	AAU99631	Mouse sec
27	49	11.3	50	2	AAU12405	Human 5'
28	48.5	11.2	40	2	AAO88860	Peptide t
29	48.5	11.2	40	8	ADS07403	Staphyloc
30	48	11.1	19	2	AAO75547	P. Commun
31	48	11.1	20	2	AAO80845	HIV pepti
32	48	11.1	48	8	ABO55454	Human gen
33	48	11.1	50	4	AAU44389	Propionib
34	48	11.1	50	6	ABM40908	Human bre
35	47.5	11.0	46	4	AAO63400	Human ORF
36	47.5	11.0	50	5	ABP35345	Human ORF
37	47	10.9	23	6	ABR91640	P. papata
38	46.5	10.8	38	2	AAU11409	Human 5'
39	46.5	10.8	46	4	AAO96710	Human rep
40	46.5	10.8	46	4	AAU22911	Human pro
41	46.5	10.8	46	7	ADJ09484	Human pro
42	46	10.6	20	2	AAO45839	Peptide r
43	46	10.6	26	2	AAV31378	Human pro
44	46	10.6	30	6	AAE34173	T-cell st
45	46	10.6	38	8	ADP73905	Human ant

ALIGNMENTS

RESULT 1
AAO26686
ID AAO26686 standard; peptide; 18 AA.
XX
AC AAO26686;
XX
DT 20-MAR-2003 (first entry)
XX
DE Human KIM-1 mucin domain related peptide, SEQ ID No 14.
XX
KW Cytostatic; gene therapy; antibody; antigen; antigen-binding;
KW proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;
KW renal disease; injury; renal cancer.
XX
OS Synthetic.
XX
PN WO200298920-A1.
XX
PD 12-DEC-2002.
XX
PF 31-MAY-2002; 2002WO-US017402.
XX
PR 01-JUN-2001; 2001US-0295449P.
PR 04-JUN-2001; 2001US-0295907P.
(BIOJ) BIOGEN INC.
(GEO) GEN HOSPITAL CORP.
Baillly V, Bonventre J;
WPI; 2003-156845/15.
New antibody, antibody derivative or antigen-binding polypeptide that
inhibits proteolytic release of a soluble kidney injury molecule-1
polypeptide, useful for treating or preventing renal disease or injury,
e.g. renal cancer.
Disclosure; Fig 1A; 42pp; English.
The invention relates to a novel antibody, antibody derivative or antigen
-binding polypeptide that inhibits proteolytic release of a soluble
kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.
The antibody, molecule or antigen-binding polypeptide is
useful for treating or preventing renal disease or injury, e.g. renal
cancer. The antibody is also useful for inhibiting shedding of the KIM-1
polypeptide. This sequence represents a human KIM-1 mucin domain related
peptide of the invention

```
SQ Sequence 18 AA;
  Query Match      23.4%; Score 101; DB 6; Length 18;
  Best Local Similarity 100.0%; Pred. No. 0.002;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 46 TDGNDVTVTSSDGLWNNN 63
  |||||
DB 1 TDGNDVTVTSSDGLWNNN 18
  |||||

RESULT 2
AAO26687
ID AAO26687 standard; peptide; 18 AA.
XX
AC AAO26687;
XX
DT 20-MAR-2003 (first entry)
DE Human KIM-1 mucin domain related peptide, SEQ ID No 15.
XX
DE Human KIM-1 mucin domain related peptide, SEQ ID No 15.
XX
XX Cytostatic; gene therapy; antibody; antigen; antigen-binding;
KW proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;
KW renal disease; injury; renal cancer.
XX
OS Synthetic.
XX
PN WO200298920-A1.
XX
PD 12-DEC-2002.
XX
PF 31-MAY-2002; 2002WO-US017402.
XX
PR 01-JUN-2001; 2001US-0295449P.
XX
PR 04-JUN-2001; 2001US-0295907P.
XX
XX (BIOJ ) BIOGEN INC.
PA (GEHO ) GEN HOSPITAL CORP.
XX
XX Baillly V, Bonventre J;
XX
XX WPI; 2003-156845/15.
XX
XX New antibody, antibody derivative or antigen-binding polypeptide that
PT inhibits proteolytic release of a soluble kidney injury molecule-1
PT polypeptide, useful for treating or preventing renal disease or injury,
PT e.g. renal cancer.
XX
PS Claim 4; Page 25; 42pp; English.
XX
CC The invention relates to a novel antibody, antibody derivative or antigen
CC -binding polypeptide that inhibits proteolytic release of a soluble
CC kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.
CC The antibody, antibody derivative or antigen-binding polypeptide is
CC useful for treating or preventing renal disease or injury, e.g. renal
CC cancer. The antibody is also useful for inhibiting shedding of the KIM-1
CC polypeptide. This sequence represents a binding epitope of the invention
XX
SQ Sequence 18 AA;
  Query Match      22.9%; Score 99; DB 6; Length 18;
  Best Local Similarity 100.0%; Pred. No. 0.0032;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 55 SSDGLWNNNTQFLFHS 72
  |||||
DB 1 SSDGLWNNNTQFLFHS 18
  |||||

RESULT 4
AAO26681
ID AAO26681 standard; peptide; 18 AA.
XX
AC AAO26681;
XX
DT 20-MAR-2003 (first entry)
DE Human KIM-1 mucin domain related peptide, SEQ ID No 9.
XX
XX Cytostatic; gene therapy; antibody; antigen; antigen-binding;
KW proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;
KW renal disease; injury; renal cancer.
XX
OS Synthetic.
XX
PN WO200298920-A1.
XX
```



```

CC peptide of the invention
XX Sequence 18 AA;
SQ
  Query Match      22.2%; Score 96; DB 6; Length 18;
  Best Local Similarity 100.0%; Pred. No. 0.0065;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 QPAETHPTTLOGAIRREP 36
Db 1 QPAETHPTTLOGAIRREP 18
  |||||
  |||||

RESULT 7
AAO26685
ID AAO26685 standard; peptide; 18 AA.
XX
AC AAO26685;
XX
XX 20-MAR-2003 (first entry)
XX
DE Human KIM-1 mucin domain related peptide, SEQ ID No 13.
XX
XX Cytostatic; gene therapy; antibody; antigen; antigen-binding;
XX proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;
XX renal disease; injury; renal cancer.
XX
OS Synthetic.
XX
XX WO200298920-A1.
XX
XX 12-DEC-2002.
XX
XX 31-MAY-2002; 2002WO-US017402.
XX
XX 01-JUN-2001; 2001US-0295449P.
XX 04-JUN-2001; 2001US-0295907P.
XX
XX (BIOJ ) BIOGEN INC.
XX (GEO ) GEN HOSPITAL CORP.
XX
XX Bailly V, Bonventre J;
XX
XX WPI; 2003-156845/15.
XX
XX New antibody, antibody derivative or antigen-binding polypeptide that
XX inhibits proteolytic release of a soluble kidney injury molecule-1
XX polypeptide, useful for treating or preventing renal disease or injury,
XX e.g. renal cancer.
XX
XX Disclosure; Fig 1A; 42pp; English.
XX
XX The invention relates to a novel antibody, antibody derivative or antigen
XX -binding polypeptide that inhibits proteolytic release of a soluble
XX kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.
XX The antibody, antibody derivative or antigen-binding polypeptide is
XX useful for treating or preventing renal disease or injury, e.g. renal
XX cancer. The antibody is also useful for inhibiting shedding of the KIM-1
XX polypeptide. This sequence represents a human KIM-1 mucin domain related
XX peptide of the invention
XX
XX Sequence 18 AA;
XX
  Query Match      21.3%; Score 92; DB 6; Length 18;
  Best Local Similarity 100.0%; Pred. No. 0.017;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 LQGAIRREPTSSPLYSYT 45
Db 1 LQGAIRREPTSSPLYSYT 18
  |||||
  |||||

RESULT 9
AAO26688
ID AAO26688 standard; peptide; 18 AA.
XX
XX AAO26688;
XX
XX 20-MAR-2003 (first entry)
XX
XX Human KIM-1 mucin domain related peptide, SEQ ID No 16.
XX
XX Cytostatic; gene therapy; antibody; antigen; antigen-binding;
XX proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;
XX renal disease; injury; renal cancer.
XX
OS Synthetic.

```

XX PN WO200298920-A1.
 XX PD 12-DEC-2002.
 XX PF 31-MAY-2002; 2002WO-US017402.
 XX PR 01-JUN-2001; 2001US-0295449P.
 XX PR 04-JUN-2001; 2001US-0295907P.
 XX PA (BIOJ) BIOGEN INC.
 XX PA (GEO) GEN HOSPITAL CORP.
 XX PI Bailly V, Bonventre J;
 XX WI WIPI; 2003-156845/15.
 XX New antibody, antibody derivative or antigen-binding polypeptide that
 PT inhibits proteolytic release of a soluble kidney injury molecule-1
 PT polypeptide, useful for treating or preventing renal disease or injury,
 PT e.g. renal cancer.
 XX Disclosure; Fig 1A; 42pp; English.
 XX The invention relates to a novel antibody, antibody derivative or antigen
 CC -binding polypeptide that inhibits proteolytic release of a soluble
 CC kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.
 CC The antibody, antibody derivative or antigen-binding polypeptide is
 CC useful for treating or preventing renal disease or injury, e.g. renal
 CC cancer. The antibody is also useful for inhibiting shedding of the KIM-1
 CC polypeptide. This sequence represents a human KIM-1 mucin domain related
 CC peptide of the invention
 XX Sequence 18 AA;
 XX
 XX Query Match 20.8%; Score 90; DB 6; Length 18;
 XX Best Local Similarity 100.0%; Pred. No. 0.027;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 64 QTQLFLEHSLLTANTTKG 81
 DB 1 QTQLFLEHSLLTANTTKG 18
 RESULT 10
 AAM20331
 ID AAM20331 standard; protein; 50 AA.
 AC AAM20331;
 XX 12-OCT-2001 (first entry)
 XX Peptide #6765 encoded by probe for measuring cervical gene expression.
 XX Probe; human; microarray; gene expression; cervical epithelial cell;
 XX cervical cancer.
 XX Homo sapiens.
 XX WO200157278-A2.
 XX 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US000670.
 XX 04-FEB-2000; 2000US-0180312P.
 XX 26-MAY-2000; 2000US-0207456P.
 XX 30-JUN-2000; 2000US-00608408.
 XX 03-AUG-2000; 2000US-00632366.
 XX 21-SEP-2000; 2000US-0234687P.
 XX 27-SEP-2000; 2000US-0236359P.
 XX 04-OCT-2000; 2000GB-00024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WIPI; 2001-483447/52.
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human fetal liver.
 XX Claim 27; SEQ ID NO 33500; 639pp + Sequence Listing; English.
 XX The invention relates to a single exon nucleic acid probe for measuring

PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WIPI; 2001-488901/53.
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human cervical epithelial cells.
 XX Claim 27; SEQ ID NO 25157; 487pp; English.
 XX The present invention relates to human single exon nucleic acid probes
 CC (SENPs: see AAI10068-AA128459). The present sequence is a peptide encoded
 CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
 CC can be used to produce a single exon microarray, which can be used for
 CC measuring human gene expression in a sample derived from human cervical
 CC epithelial cells. By measuring gene expression, the probes are therefore
 CC useful in grading and/or staging of diseases of the cervix, notably
 CC cervical cancer. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 50 AA;
 SQ
 Query Match 13.9%; Score 60; DB 4; Length 50;
 XX Best Local Similarity 44.4%; Pred. No. 1.1e+02;
 XX Matches 16; Conservative 3; Mismatches 9; Indels 8; Gaps 2;
 QY 12 ATSPSS-----PPAETHPTTLOGAIRREPTSSP 40
 DB 5 ATSPSSRAAFTAPPTVAPTACPGAVPR-FTTTP 39
 RESULT 11
 ABB40865
 ID ABB40865 standard; peptide; 50 AA.
 XX ABB40865;
 XX 04-FEB-2002 (first entry)
 XX Peptide #8371 encoded by human foetal liver single exon probe.
 XX Human; foetal liver; gene expression; single exon nucleic acid probe.
 XX Homo sapiens.
 XX WO200157277-A2.
 XX 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US000669.
 XX 04-FEB-2000; 2000US-0180312P.
 XX 26-MAY-2000; 2000US-0207456P.
 XX 30-JUN-2000; 2000US-00608408.
 XX 03-AUG-2000; 2000US-00632366.
 XX 21-SEP-2000; 2000US-0234687P.
 XX 27-SEP-2000; 2000US-0236359P.
 XX 04-OCT-2000; 2000GB-00024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WIPI; 2001-483447/52.
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human fetal liver.
 XX Claim 27; SEQ ID NO 33500; 639pp + Sequence Listing; English.
 XX The invention relates to a single exon nucleic acid probe for measuring


```

AC AM74520;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 34826.
XX
XX Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma.
XX
OS Homo sapiens.
XX
PN WO200157276-A2.
XX
PD 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US0006568.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488900/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human bone marrow.
XX
XX Example 4; SEQ ID NO 34826; 658pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is a
CC protein encoded by one of the probes of the invention
XX
XX Sequence 50 AA;
XX
Query Match 13.9%; Score 60; DB 4; Length 50;
Best Local Similarity 44.4%; Pred. No. 1.1e+02;
Matches 16; Conservative 3; Mismatches 9; Indels 8; Gaps 2;

OY 12 ATSPSS-----PQPAETHPTTLOGAIRREPTSSP 40
DB 5 ATSPSSRAAPTLPAPPTVAPTACPGAVPR-PTTTP 39

RESULT 15
ANM61724.
ID ANM61724 standard; protein; 50 AA.
XX
AC ANM61724;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 33829.
XX
KW Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX

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PF 30-JAN-2001; 2001WO-US0006667.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT brains.
XX
PS Example 4; SEQ ID NO 33829; 650pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention
XX
XX Sequence 50 AA;
XX
Query Match 13.9%; Score 60; DB 4; Length 50;
Best Local Similarity 44.4%; Pred. No. 1.1e+02;
Matches 16; Conservative 3; Mismatches 9; Indels 8; Gaps 2;

OY 12 ATSPSS-----PQPAETHPTTLOGAIRREPTSSP 40
DB 5 ATSPSSRAAPTLPAPPTVAPTACPGAVPR-PTTTP 39

Search completed: June 29, 2005, 09:41:02
Job time : 58.3792 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 09:27:45 ; Search time 10.8212 Seconds
(without alignments)
720.211 Million cell updates/sec

Title: US-10-718-321-6
Perfect score: 432
Sequence: 1 MPLPRQNHPEVATSPSPQP.....NNQTQLFLESLLTANTTKG 81

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 11837

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	13.2	42	2	glycoprotein Ib al
2	51	11.8	43	2	hypothetical 5.2K
3	47.5	11.0	46	2	arabinogalactan pr
4	47.5	11.0	47	2	hypothetical prote
5	43.5	10.1	49	2	ig mu chain transm
6	43	10.0	31	2	hypothetical prote
7	43	10.0	35	2	aminoglycoside N6'
8	43	10.0	42	2	extensin - tomato
9	42.5	9.8	46	2	pol protein - simi
10	42	9.7	41	2	hypothetical prote
11	40.5	9.4	25	2	canA protein (IgA)
12	40.5	9.4	32	2	histone H1 - sea u
13	40.5	9.4	50	2	hypothetical prote
14	39.5	9.1	47	2	androgen-binding p
15	39	9.0	30	2	hypothetical prote
16	39	9.0	42	2	lipoprotein vsaH l
17	38	8.8	36	2	collagen alpha 1(X
18	38	8.6	48	2	hypothetical prote
19	37	8.6	31	2	hypothetical prote
20	37	8.6	34	2	ribulose-bisphosph
21	37	8.6	44	2	hypothetical prote
22	37	8.6	45	2	ig alpha chain, tr
23	37	8.6	47	2	hypothetical prote
24	37	8.6	48	2	superoxide dismuta
25	37	8.6	50	2	mucin - sheep (fra
26	36.5	8.4	22	2	histone H1 - sea u
27	36.5	8.4	36	2	histone H1 - sea u
28	36.5	8.4	46	2	pol protein - simi
29	36.5	8.4	47	2	sepiapterin reduct

troponin T 2fa - r
androgen-binding p
phospholipase A2 (
hypothetical prote
coagulation factor
t-complex polypept
outer membrane pro
biotin-binding pro
hypothetical prote
histone H5 - pigeo
hypothetical prote
gamma-hordein 3 -
beta-fructofuranos
ATP synthase beta-
translation initia
hypothetical prote

ALIGNMENTS

RESULT 1

I70082

glycoprotein Ib alpha variant B - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004

C;Accession: I70082

R;Lopez, J.A.; Ludwig, E.H.; McCarthy, B.J.

J. Biol. Chem. 267, 10055-10061, 1992

A;Title: Polymorphism of human glycoprotein Ib alpha results from a variable number of t ations.

A;Reference number: I55355; MUID:92250564; PMID:1577776

A;Accession: I70082

A;Status: preliminary; translated from GE/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-42 <RES>

A;Cross-references: UNIPROT:Q16469; GB:S34439; NID:G249178; PIDN:AAB22153.1; PID:G249178

C;Superfamily: platelet glycoprotein Ib alpha chain; leucine-rich alpha-2-glycoprotein r

C;Keywords: glycoprotein

Query Match 13.2%; Score 57; DB 2; Length 42;
Best Local Similarity 43.9%; Pred. No. 26;
Matches 18; Conservative 3; Mismatches 10; Indels 10; Gaps 3;

Qy 9 EPVATSPSPQPAE---THPTTLQGAIRREPTSPLYSYTT 46

Db 5 EP-APSPTEPTSEPAPSPPT-----PEPTSEPAPSPPT 38

RESULT 2

JU0404

hypothetical 5.2K protein - clover yellow mosaic virus

C;Species: clover yellow mosaic virus

C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004

C;Accession: JU0404

R;Abouhaider, M.G.; Lai, R.

J. Gen. Virol. 70, 1871-1875, 1989

A;Title: Nucleotide sequence of the 3'-terminal region of clover yellow mosaic virus RNA

A;Reference number: JU0402; MUID:89293092; PMID:2738582

A;Accession: JU0404

A;Molecule type: genomic RNA

A;Residues: 1-43 <ABO>

A;Cross-references: UNIPROT:P16485; GB:D00485; NID:G221218; PIDN:BA00374.1; PID:d100082

A;Note: this protein is encoded by sequence in front of the coat protein-encoding sequen

Query Match 11.8%; Score 51; DB 2; Length 43;
Best Local Similarity 45.8%; Pred. No. 1e+02;
Matches 11; Conservative 3; Mismatches 6; Indels 4; Gaps 1;

Qy 4 PRONHEPVATSPSPQPAETHPTT 27

Db 20 PRQSHLPQAT-----PQRLSYPKT 39

R;van der Eycken, W.; de Almeida Engler, J.; Inze, D.; van Montagu, M.; Gheysen, G.
Plant J. 9, 45-54, 1996
A;Title: A molecular study of Meloidogyne incognita-induced feeding sites.
A;Reference number: 215873; MUID:96158345; PMID:8580972
A;Accession: T07030
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-42 <VAN>
A;Cross-references: UNIPROT:Q40145; EMBL:Z46675; NID:G575949; PIDN:CAA86660.1; PID:G575949
A;Experimental source: strain Marmande; Meloidogyne incognita-induced root knot
C;Superfamily: hydroxyproline-rich glycoprotein
C;Keywords: cell wall; glycoprotein; hydroxyproline

Query Match 10.0%; Score 43; DB 2; Length 42;
Best Local Similarity 29.7%; Pred. No. 6.1e+02;
Matches 11; Conservative 2; Mismatches 12; Indels 12; Gaps 1;

Qy 10 PVATSPSSPPQPAETHPTTLQGAIRREPTSSPLYSYTT 46
Db 11 PIYKSPPTPAYNSP-----PPPYLYTYS 35

RESULT 9
A49281
pol protein - simian T-cell lymphotropic virus type 1, STLV-1 (isolate Bab34) (fragment)
C;Species: simian T-cell lymphotropic virus type 1, STLV-1
C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004
C;Accession: A49281
R;Saksena, N.K.; Herve, V.; Durand, J.P.; Lequenne, B.; Diop, O.M.; Digoutte, J.P.; Math
Paul, B.; Dube, D.K.; Barre-Sinoussi, F.; Poesz, B.J.
Virology 198, 297-310, 1994
A;Title: Seroprevalence, molecular, and phylogenetic analyses of simian T-cell leukemia virus type 1 (STLV-1) in human populations.
A;Reference number: A49281; MUID:94082462; PMID:8259665
A;Accession: A49281
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-46 <SAK>
A;Cross-references: UNIPROT:Q88390; GB:L20351; NID:G431689; PIDN:AAA16596.1; PID:G431690
C;Superfamily: pol polyprotein

Query Match 9.8%; Score 42.5; DB 2; Length 46;
Best Local Similarity 39.4%; Pred. No. 7.6e+02;
Matches 13; Conservative 3; Mismatches 14; Indels 3; Gaps 2;

Qy 41 LYSYTTDGNVTVES--SDGLMNNQTLFLEH 71
Db 13 LYKYFTDKPLMDNALSIGLWTFHNLNV-LTH 44

RESULT 10
C87603
hypothetical protein CC2859 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: C87603
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: C87603
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-41 <STO>
A;Cross-references: UNIPROT:Q9A4H5; GB:AE005673; NID:G13424473; PIDN:AAK24823.1; GSPDB:G
C;Genetics:

Query Match 9.7%; Score 42; DB 2; Length 41;
Best Local Similarity 29.6%; Pred. No. 7.4e+02;
Matches 8; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

Qy 4 PRNHPEVATSPSSPPQPAETHPTTLQ 30
Db 12 PKGLNDRSTGGQPPRPPIPDALRG 38

RESULT 11
I40692
cena protein (Iga1h) - Cellulomonas fimi (fragment)
C;Species: Cellulomonas fimi
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 22-Oct-1999
C;Accession: I40692
R;Miller, P.B.; Shen, H.; Gilkes, N.R.; Kilburn, D.G.; Miller, R.C.; Plaut, A.G.; Warren
FEMS Microbiol. Lett. 92, 199-204, 1992
A;Title: Endoglucanase A from Cellulomonas fimi in which the hinge sequence of human Iga
hosea.
A;Reference number: I40692
A;Accession: I40692
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-25 <RES>
A;Cross-references: EMBL:X65780; NID:G312035; PIDN:CAA46663.1; PID:G312036

Query Match 9.4%; Score 40.5; DB 2; Length 25;
Best Local Similarity 32.4%; Pred. No. 5.7e+02;
Matches 12; Conservative 1; Mismatches 7; Indels 17; Gaps 1;

Qy 10 PVATSPSSPPQPAETHPTTLQGAIRREPTSSPLYSYTT 46
Db 6 PPTSPSTP-----PTPSPLQSNVT 25

RESULT 12
B38839
histone H1 - sea urchin (Strongylocentrotus intermedius) (fragment)
C;Species: Strongylocentrotus intermedius
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: B38839
R;Suzuki, M.; Sugiyama, M.; Ebashi, S.
J. Biochem. 108, 347-355, 1990
A;Title: Sea urchin protease specific to the SPKK motif in histone.
A;Reference number: PS0145; MUID:91115778; PMID:2126010
A;Accession: B38839
A;Molecule type: protein
A;Residues: 1-32 <SUZ>
A;Cross-references: UNIPROT:Q7M407
C;Superfamily: histone H1
C;Keywords: chromosomal protein; nucleosome

Query Match 9.4%; Score 40.5; DB 2; Length 32;
Best Local Similarity 38.5%; Pred. No. 7.7e+02;
Matches 10; Conservative 1; Mismatches 8; Indels 7; Gaps 1;

Qy 15 PSSPPQPAETHPTTLQGAIRREPTSSP 40
Db 1 PASPQKRAASP-----RSPKSP 19

RESULT 13
AH2135
hypothetical protein asl2639 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AH2135
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AH2135
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-50 <KUR>

A;Cross-references: UNIPROT:Q8VTS4; GB:BA000019; PIDN:BA874338.1; PID:g17131732; GSPDB:G17131732
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: asl2639

Query Match 9.4%; Score 40.5; DB 2; Length 50;
Best Local Similarity 27.0%; Pred.No.1.3e+03;
Matches 10; Conservative 5; Mismatches 19; Indels 3; Gaps 1;

Qy 7 NHEPVATSPSPQPAETHP---TTLQAIRREPTSSP 40
Db 10 NNTKTPNNPTKPKKLLHPKLOTHPNLKNSTKSP 46

RESULT 14

A40703
androgen-binding protein ABP (N-terminal, exon A) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A40703
R:Sullivan, P.M.; Wang, Y.M.; Joseph, D.R.
Mol. Endocrinol. 7, 702-715, 1993
A:Title: Identification of an alternate promoter in the rat androgen-binding protein/sex
tion.
A:Reference number: A40703; MUID:93302779; PMID:7686253
A:Accession: A40703
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-47 <SUI>
A:Cross-references: UNIPROT:Q08946; GB:U85959; GB:S62931; NID:G1872518; PIDN:AAB49304.1;
A:Note: sequence extracted from NCBI backbone (NCBIN:134229, NCBIPI:134230)

Query Match	9.1%	Score 39.5;	DB 2;	Length 47;
Best Local Similarity	42.3%	Pred. No. 1.5e+03;		
Matches 11;	Conservative	3;	Mismatches 11;	Indels 1;
Matches 1;	Gaps	1;	Gaps	1;

Qy	11	VATSSS-FQPAETHPTTLOGAIRRE	35
		:	
Db	6	VPLQSTVVPSPRPPTTLEANQSR	31

RESULT 15

D82251
hypothetical protein VC1030 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)
C:Species: *Vibrio cholerae*
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: D8251
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A>Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: D82251
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-30 <HEI>
A:Cross-references: UNIPROT:Q9K775; GB:AE004184; GB:AE003852; NID:g9655483; PIDN:AAF9418
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC1030
A:Map position: 1

Query Match	9.0%	Score 39;	DB 2;	Length 30;
Best Local Similarity	61.5%	Pred. No. 9.9e+02;		
Matches 8;	Conservative	0;	Mismatches 5;	Indels
				0;
				Gaps
				0;

Qy	67	L	F	L	E	H	S	L	L	T	A	N	T	T	79
Db	12	L	F	E	H	E	L	L	R	I	N	V	T	24	

Result No.	Query #				DB	ID	Description
	Score	Match	Length				
1	51	11.8	43	1	Y5K	CYMW	P16485 clover yell
2	48	11.1	30	2	Q7THH6		Q7thh6 human adeno
3	47.5	11.0	46	2	Q7WLG3		Q7wmj3 lolium mult
4	47.5	11.0	47	2	Q8YFV1		Q8yfv1 brucella me
5	47	10.9	43	2	Q86LU3		Q86lu3 cryptospori
6	46	10.6	43	2	Q81OR6		Q81or6 cryptospori
7	46	10.6	43	2	Q81OR7		Q81or7 cryptospori
8	46	10.6	43	2	Q81SB4		Q81sb4 cryptospori
9	46	10.6	49	2	Q82954		Q82954 rai1stonia s
10	46	10.6	50	2	Q7UVZ0		Q7uvz0 rhodopirell
11	45.5	10.5	48	2	Q6WV04		Q6wv04 saccharomyc
12	45	10.4	32	2	Q9FNP3		Q9fnp3 arabidopsis
13	44.5	10.3	49	2	Q91FZ1		Q91fz1 chilo iridee
14	44.5	10.3	49	2	Q8J415		Q8j415 chimpanzee
15	44	10.2	43	2	Q86LU1		Q86lu1 cryptospori
16	44	10.2	43	2	Q86LU6		Q86lu6 cryptospori
17	44	10.2	46	2	Q8J418		Q8j418 chimpanzee
18	44	10.2	46	2	Q8J4J7		Q8j4j7 chimpanzee
19	44	10.2	47	2	Q8J4I9		Q8j4i9 chimpanzee
20	44	10.2	49	2	Q8BBA2		Q8bba2 human respi
21	43.5	10.1	41	2	Q99J74		Q99jt4 mus musculu
22	43.5	10.1	47	2	Q8J4H7		Q8j4h7 chimpanzee
23	43	10.0	30	2	Q7THC7		Q7thc7 human adeno
24	43	10.0	30	2	Q7THH4		Q7thh4 human adeno
25	43	10.0	30	2	Q7THH5		Q7thh5 human adeno
26	43	10.0	30	2	Q7THH7		Q7thh7 human adeno
27	43	10.0	30	2	Q7THH8		Q7thh8 human adeno
28	43	10.0	30	2	Q7THH9		Q7thh9 human adeno
29	43	10.0	30	2	Q7THI0		Q7thi0 human adeno
30	43	10.0	30	2	Q7THI1		Q7thi1 human adeno
31	43	10.0	30	2	Q7THI2		Q7thi2 human adeno

```

[1]
RP SEQUENCE FROM N.A.
RA Lee C., Lee S.-H., Han E., Kim S.-J.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR ENBL; AY280886; AAP43056.1; -.
DR HSSP; P03277; 1P2Z.
DR GO; GO:0019028; C:virial capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000736; Adeno_hexon.
DR Pfam; PF01065; Adeno_hexon; 1.
DR ProDom; PD002815; Adeno_hexon; 1.
FT NON_TER 1
FT NON_TER 30
SQ SEQUENCE 30 AA; 3450 MW; 531F6P951E27039B CRC64;

Query Match 11.1%; Score 48; DB 2; Length 30;
Best Local Similarity 45.0%; Pred. No. 8.5e+02;
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 34 REPTSPLYSYTTDNDTVT 53
DB 5 RNPTVPTDVTDRSRLT 24

RESULT 3
Q7M1G3 PRELIMINARY; PRT; 46 AA.
AC Q7M1G3;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Arabinogalactan protein (Fragments).
OS Lolium multiflorum (Italian Ryegrass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Poace; Lolium.
OX NCBI_TaxID=4521;
RN [1]
RP SEQUENCE.
RX MEDLINE=90147544; PubMed=2695069;
RA Gleeson P.A., McNamara M., Wattenhall R.E.H., Stone B.A.,
RA Fincher G.B.;
RT "Characterization of the hydroxyproline-rich protein core of an
RT arabinogalactan-protein secreted from suspension-cultured Lolium
RT multiflorum (Italian ryegrass) endosperm cells.";
RL Biochem. J. 264:1857-862(1989).
DR PIR; S07073; S07073.
DR NON_TER 1
DR NON_TER 46
SQ SEQUENCE 46 AA; 4173 MW; EF61188B0C8A08D0 CRC64;

Query Match 11.0%; Score 47.5; DB 2; Length 46;
Best Local Similarity 47.8%; Pred. No. 1.6e+03;
Matches 11; Conservative 2; Mismatches 7; Indels 3; Gaps 1;

QY 2 PLRQNHPEVA---TSPSSPPA 21
DB 18 FVPEASTAPVAAPTXXSPSPA 40

RESULT 4
Q8YFV1 PRELIMINARY; PRT; 47 AA.
AC Q8YFV1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein BMEI1419.
GN OrderedLocustNames=BMEI1419.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;

[1]
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; PubMed=11756688; DOI=10.1073/pnas.221575398;
RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mijer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haeckelorn R., Kyrpides N.C., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
DR EMBL; AE009579; AAL52600.1; -.
DR PIR; AE3429; AE3429.
KW Complete proteome.
SQ SEQUENCE 47 AA; 5180 MW; 989EE40500EC57D0 CRC64;

Query Match 11.0%; Score 47.5; DB 2; Length 47;
Best Local Similarity 45.9%; Pred. No. 1.6e+03;
Matches 17; Conservative 3; Mismatches 12; Indels 5; Gaps 3;

QY 4 PRONHEPVATSP--SSQPAETHP-TTLQCAIRREPT 37
DB 12 PRP--DAVLRSPDSDSAPQPAATAPNTTQNRWRELKT 46

RESULT 5
Q86LU3 PRELIMINARY; PRT; 43 AA.
AC Q86LU3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein (Fragment).
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=870;
RX MEDLINE=22511025; PubMed=12624019;
RA Leon F., Gallimore C.I., Green J., McLauchlin J.;
RT "Molecular epidemiological analysis of Cryptosporidium isolates from
RT humans and animals by using a heteroduplex mobility assay and nucleic
RT acid sequencing based on a small double-stranded RNA element.";
RL J. Clin. Microbiol. 41:981-992(2003).
DR EMBL; AY176656; AA019461.1; -.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 43
SQ SEQUENCE 43 AA; 4750 MW; 1D0A81C40B323D35 CRC64;

Query Match 10.9%; Score 47; DB 2; Length 43;
Best Local Similarity 33.3%; Pred. No. 1.6e+03;
Matches 12; Conservative 10; Mismatches 10; Indels 4; Gaps 2;

QY 44 YTTDNDTFTSSDGL---WNNNTQLFLEHSLTA 76
DB 3 FVTDLSDLSNTADGLGQAW-YKISQVAIEHILTA 37

RESULT 6
Q81OR6 PRELIMINARY; PRT; 43 AA.
AC Q81OR6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
```


[illegible]

the genome of insect iridescent virus type 6 between the genome
coordinates 0.310 and 0.347 (7990 bp).";
RL Intervirolgy 37:287-297(1994).
[6]
RN SEQUENCE FROM N.A.
RX MEDLINE=98141693; PubMed=9482589; DOI=10.1023/A:1007932620930;
RA Bahr U., Tidona C.A., Darai G.;
RA "The DNA sequence of Chilo iridescent virus between the genome
coordinates 0.101 and 0.391; similarities in coding strategy between
insect and vertebrate iridoviruses.";
RN Virus Genes 15:235-245(1997).
[7]
RN SEQUENCE FROM N.A.
RA Delius H., Darai G., Fluegel R.M.;
RT "DNA analysis of insect iridescent virus 6: evidence for circular
permutation and terminal redundancy.";
RL J. Virol. 49:609-614(1984).
[8]
RN SEQUENCE FROM N.A.
RX MEDLINE=86174607; PubMed=3959991;
RA Lorbacher de Ruiz H., Gelderblom H., Hofmann W., Darai G.;
RT "Insect iridescent virus type 6 induced toxic degenerative hepatitis
in mice.";
RL Med. Microbiol. Immunol. 175:43-53(1986).
[9]
RN SEQUENCE FROM N.A.
RX MEDLINE=87321126; PubMed=2820141;
RA Schnitzler P., Soltan J.B., Fischer M., Reisner H., Scholz J.,
RA Delius H., Darai G.;
RT "Molecular cloning and physical mapping of the genome of insect
iridescent virus type 6: further evidence for circular permutation of
the viral genome.";
RL Virology 160:66-74(1987).
[10]
RN SEQUENCE FROM N.A.
RX MEDLINE=89073752; PubMed=3201750;
RA Fischer M., Schnitzler P., Delius H., Darai G.;
RT "Identification and characterization of the repetitive DNA element in
the genome of insect iridescent virus type 6.";
RL Virology 167:485-496(1988).
[11]
RN SEQUENCE FROM N.A.
RX MEDLINE=92196996; PubMed=1549908;
RA Handermann M., Schnitzler P., Rosen-Wolff A., Raab K., Sonntag K.C.,
RA Darai G.;
RT "Identification and mapping of origins of DNA replication within the
DNA sequences of the genome of insect iridescent virus type 6.";
RL Virus Genes 6:19-32(1992).
[12]
RN SEQUENCE FROM N.A.
RX MEDLINE=93260401; PubMed=8492091;
RA Stohwasser R., Raab K., Schnitzler P., Janssen W., Darai G.;
RT "Identification of the gene encoding the major capsid protein of
insect iridescent virus type 6 by polymerase chain reaction.";
RL J. Gen. Virol. 74:873-879(1993).
[13]
RN SEQUENCE FROM N.A.
RX MEDLINE=94167241; PubMed=8121799;
RA Schnitzler P., Hug M., Handermann M., Janssen W., Koonin E.V.,
RA Delius H., Darai G.;
RT "Identification of genes encoding zinc finger proteins, non-histone
chromosomal HMG protein homologue, and a putative GTP phosphohydrolase
in the genome of Chilo iridescent virus.";
RL Nucleic Acids Res. 22:158-166(1994).
[14]
RN SEQUENCE FROM N.A.
RX MEDLINE=99383793; PubMed=10456793; DOI=10.1023/A:1008072319875;
RA Muller K., Tidona C.A., Darai G.;
RT "Identification of a gene cluster within the genome of Chilo
iridescent virus encoding enzymes involved in viral DNA replication
and processing.";
RL Virus Genes 18:243-264(1999).
[15]

RP	SEQUENCE FROM N.A.
RX	MEDLINE=21342589; PubMed=11448171; DOI=10.1006/viro.2001.0963;
RA	Jacob N.J., Muller K., Bahr U., Darai G.;
RT	"Analysis of the first complete DNA sequence of an iridovirus"
RL	iridovirus: coding strategy of the genome of Chilo iridescent virus.";
RE	Virology 286:182-196(2001).
DR	EMBL; AF303741; AAK82041.1; -
SQ	SEQUENCE 49 AA; 5458 MW; 744BBC42765D078 CRC64;
Query Match	10.3%; Score 44.5; DB 2; Length 49;
Best Local Similarity	31.9%; Pred. No. 3.3e+03;
Matches	15; Conservative 5; Mismatches 16; Indels 11; Gaps
Oy	37 TSSPLY---SYTTGDNDVTSSDGLMNNOTQLFLEHSLLTANTTK 80
Dd	4 TTPSYKTPSYKTPSYKYTVT-----NSGAKIPSSHNSSTNNSTK 42
RESULT 14	
O8J4I5	PRELIMINARY; PRT; 49 AA.
ID O8J4I5	
AC O8J4I5	
DT 01-OCT-2002	(TrEMBLrel. 22, Created)
DT 01-OCT-2002	(TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003	(TrEMBLrel. 23, Last annotation update)
DE	Envelope glycoprotein (Fragment).
OS	Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
OC	Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX	NCBI_TaxID=11723;
RN [1]	
RP	SEQUENCE FROM N.A.
RX	Trichel A.M., Rajakumar P.A., Murphey-Corb M.A.;
RL	Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AY118212; AAM78572.1; -
GO	GO: 0019031; C:viral envelope; IEA.
KW	Envelope protein.
FT NON TER	1
FT NON TER	49
SQ	SEQUENCE 49 AA; 5101 MW; 86D35EBE15D4FC94 CRC64;
Query Match	10.3%; Score 44.5; DB 2; Length 49;
Best Local Similarity	39.5%; Pred. No. 3.3e+03;
Matches	17; Conservative 4; Mismatches 17; Indels 5; Gaps
Oy	25 PTTLOGAIRRETSPPLSYTYTGGNDVTSSDGLMNNNOTQL 67 : : : : : :
Dd	8 PTTT--ATTKTITT---VSTTFPKADVNETSSCVKNNTCTL 45 : : : : :
RESULT 15	
O86LU1	PRELIMINARY; PRT; 43 AA.
ID O86LU1	
AC O86LU1	
DT 01-JUN-2003	(TrEMBLrel. 24, Created)
DT 01-JUN-2003	(TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003	(TrEMBLrel. 24, Last annotation update)
DE	Hypothetical protein (Fragment).
OS	Cryptosporidium parvum
OC	Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC	Cryptosporidiidae; Cryptosporidium.
OX	NCBI_TaxID=5807;
RN [1]	
RP	SEQUENCE FROM N.A.
RC STRAIN=1876;	
RA MEDLINE=12624019;	
RX Leoni F., Gallimore C.I., Green J., McLauchlin J.;	
RT "Molecular epidemiological analysis of Cryptosporidium isolates from	
RT humans and animals by using a heteroduplex mobility assay and nucleic	
RT acid sequencing based on a small double-stranded RNA element.";	
RL J. Clin. Microbiol. 41:981-992(2003).	
DR EMBL; AY176661; AAO19466.1; -	
KW Hypothetical protein.	
FT NON TER	1

FT NON_TER 43 43
SQ SEQUENCE 43 AA; 4770 MW; 130461240B2A9E35 CRC64;
Query Match 10.2%; Score 44; DB 2; Length 43;
Best Local Similarity 33.3%; Pred. No. 3.2e+03;
Matches 12; Conservative 9; Mismatches 11; Indels 4; Gaps 2;
QY 44 YTTDGNQDTVTESDGL---WNNNQTLFLEHSLTLTA 76
: || : : : || | : : : || : : : ||
Db 3 FVTDLSSDFSNADGLQAW-YKISQVAVEHILTA 37

Search completed: June 29, 2005, 09:46:13
Job time : 49.8546 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 09:09:20 ; Search time 25.332 Seconds
(without alignments)
849.017 Million cell updates/sec

Title: US-10-718-321-6_COPY_40_81

Perfect score: 225

Sequence: 1 PLYSTTGNDVTSSDGL.....NNQTQLFLEHSLLTANTTKG 42

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 68540

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	20.9	43	2 Q86LU3	Q86LU3 cryptospori
2	46	20.4	43	2 Q81OR6	Q81OR6 cryptospori
3	46	20.4	43	2 Q81OR7	Q81OR7 cryptospori
4	46	20.4	43	2 Q81SB4	Q81SB4 cryptospori
5	45.5	20.2	48	2 Q6WV04	Q6WV04 saccharomyc
6	44	19.6	43	2 Q86LU1	Q86LU1 cryptospori
7	44	19.6	43	2 Q86LU6	Q86LU6 cryptospori
8	44	19.6	46	2 Q8J4I8	Q8J4I8 chimpanzee
9	44	19.6	49	2 Q8J4I5	Q8J4I5 chimpanzee
10	43.5	19.3	41	2 Q9J7T4	Q9J7T4 mus musculu
11	43	19.1	43	2 Q86LU2	Q86LU2 cryptospori
12	43	19.1	43	2 Q86LU5	Q86LU5 cryptospori
13	42.5	18.9	46	2 Q88390	Q88390 simian t-ly
14	42	18.7	43	2 Q86LU4	Q86LU4 cryptospori
15	42	18.7	46	2 Q7KYS6	Q7KYS6 homo sapien
16	42	18.7	47	2 Q8J4I9	Q8J4I9 chimpanzee
17	41.5	18.4	47	2 Q75JX4	Q75JX4 dictyosteli
18	41	18.2	29	2 Q86233	Q86233 human rotav
19	41	18.2	40	2 Q83DR8	Q83DR8 coxiella bu
20	41	18.2	41	2 Q11552	Q11552 human immu
21	40.5	18.0	49	2 Q91FZ1	Q91FZ1 chilo iride
22	40	17.8	49	2 Q7XA54	Q7XA54 gnemum gnm
23	39.5	17.6	46	2 Q82209	Q82209 human t-lym
24	39	17.3	28	2 Q998S5	Q998S5 turkey ente
25	39	17.3	30	2 Q9KT75	Q9KT75 vibrio chol
26	39	17.3	38	2 Q7RD73	Q7RD73 plasmodium
27	39	17.3	47	2 Q6SSH0	Q6SSH0 manheimia
28	39	17.3	50	2 Q7SEZ1	Q7SEZ1 neurospora
29	38.5	17.1	31	2 Q78501	Q78501 human immu
30	38.5	17.1	41	2 Q9R5W5	Q9R5W5 neisseria g
31	38	16.9	29	2 Q86237	Q86237 human rotav

32 38 16.9 29 2 Q86238 human rotav
33 38 16.9 29 2 Q86239 human rotav
34 38 16.9 38 2 Q71V48 human sapien
35 38 16.9 46 2 Q8UYK0 wheat dwarf
36 38 16.9 46 2 Q8UYK2 wheat dwarf
37 38 16.9 46 2 Q8UYK4 wheat dwarf
38 38 16.9 46 2 Q7SZJ6 accipiter n
39 38 16.9 46 2 Q7SZK0 aquila chry
40 38 16.9 46 2 Q7SZK2 circus spil
41 38 16.9 46 2 Q7SZK4 accipiter g
42 38 16.9 46 2 Q7SZK6 milvus migr
43 38 16.9 46 2 Q8J4I7 chimpanzee
44 38 16.9 46 2 Q9RNX5 human immu
45 38 16.9 50 2 Q7V009 prochloroco

ALIGNMENTS

RESULT 1
Q86LU3 PRELIMINARY; PRT; 43 AA.
AC Q86LU3;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DE Hypothetical protein (Fragment).
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=870;
RX MEDLINE=22511025; PubMed=12624019;
RA Leoni F., Gallimore C.I., Green J., McLauchlin J.;
RT "Molecular epidemiological analysis of Cryptosporidium isolates from humans and animals by using a heteroduplex mobility assay and nucleic acid sequencing based on a small double-stranded RNA element.";
RL J. Clin. Microbiol. 41:981-992(2003).
DR EMBL; AY176656; AA019461.1; -
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 43
SQ SEQUENCE 43 AA; 4750 MW; 1D0A81C40B323D35 CRC64;
Query Match 20.9%; Score 47; DB 2; Length 43;
Best Local Similarity 33.3%; Pred. No. 1.3e+02;
Matches 12; Conservative 10; Mismatches 10; Indels 4; Gaps 2;
QY 5 YTTDGNVTSSDGL---WNNQTQLFLEHSLTLTA 37
DB 3 FVTDLSLSTAGLGLGQAW-YKISOVAIEHILTLTA 37
RESULT 2
Q81OR6 PRELIMINARY; PRT; 43 AA.
AC Q81OR6;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DE Hypothetical protein (Fragment).
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1005, 1034, 1283, and 340;
RX MEDLINE=22511025; PubMed=12624019;
RA Leoni F., Gallimore C.I., Green J., McLauchlin J.;
RT "Molecular epidemiological analysis of Cryptosporidium isolates from

RT humans and animals by using a heteroduplex mobility assay and nucleic
 RT acid sequencing based on a small double-stranded RNA element.";
 RL J. Clin. Microbiol. 41:981-992(2003).

DR EMBL; AY135729; AAN62570.1; -
 DR EMBL; AY135732; AAN62573.1; -
 DR EMBL; AY135734; AAN62575.1; -
 DR EMBL; AY135735; AAN62576.1; -
 DR EMBL; AY135738; AAN62579.1; -
 DR EMBL; AY135738; AAN62579.1; -
 DR EMBL; AY176655; AAO19460.1; -
 DR EMBL; AY176657; AAO19462.1; -
 DR EMBL; AY176658; AAO19463.1; -
 DR EMBL; AY176660; AAO19465.1; -
 KW Hypothetical protein.
 FT NON_TER 1
 FT NON_TER 43
 SQ SEQUENCE 43 AA; 4736 MW; 1D0A81C40B2A9E35 CRC64;

Query Match 20.4%; Score 46; DB 2; Length 43;
 Best Local Similarity 33.3%; Pred. No. 1.7e+02;
 Matches 12; Conservative 10; Mismatches 10; Indels 4; Gaps 2;

QY 5 YTTDGNVTSSDGL---WNNQTQLFLEHLLTA 37
 : || : : : ||| | : : : ||| : |||
 Db 3 FVTDLSSDLNTADGLGQAW-YKISQVAVEHLLTA 37

RESULT 3

Q810R7 PRELIMINARY; PRT; 43 AA.
 AC Q810R7;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Cryptosporidium parvum.
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
 OC Cryptosporidiidae; Cryptosporidium.
 OX NCBI_TaxID=5807;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=T89, and 1962;
 RX MEDLINE=22511025; PubMed=12624019;
 RA Leoni F., Gallimore C.I., Green J., McLauchlin J.;
 RT "Molecular epidemiological analysis of Cryptosporidium isolates from
 RT humans and animals by using a heteroduplex mobility assay and nucleic
 RT acid sequencing based on a small double-stranded RNA element.";
 RL J. Clin. Microbiol. 41:981-992(2003).
 DR EMBL; AY135730; AAN62571.1; -
 DR EMBL; AY176652; AAO19457.1; -
 DR EMBL; AY135733; AAN62574.1; -
 DR EMBL; AY176654; AAO19459.1; -
 KW Hypothetical protein.
 FT NON_TER 1
 FT NON_TER 43
 SQ SEQUENCE 43 AA; 4766 MW; 1D0A81C40B2A8E34 CRC64;

Query Match 20.4%; Score 46; DB 2; Length 43;
 Best Local Similarity 33.3%; Pred. No. 1.7e+02;
 Matches 12; Conservative 10; Mismatches 10; Indels 4; Gaps 2;

QY 5 YTTDGNVTSSDGL---WNNQTQLFLEHLLTA 37
 : || : : : ||| | : : : ||| : |||
 Db 3 FVTDLSSDLNTADGLGQAW-YKISQVAVEHLLTA 37

RESULT 4

Q81SB4 PRELIMINARY; PRT; 43 AA.
 AC Q81SB4;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein (Fragment).

OS Cryptosporidium parvum.
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
 OC Cryptosporidiidae; Cryptosporidium.
 OX NCBI_TaxID=5807;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22511025; PubMed=12624019;
 RA Leoni F., Gallimore C.I., Green J., McLauchlin J.;
 RT "Molecular epidemiological analysis of Cryptosporidium isolates from
 RT humans and animals by using a heteroduplex mobility assay and nucleic
 RT acid sequencing based on a small double-stranded RNA element.";
 RL J. Clin. Microbiol. 41:981-992(2003).
 DR EMBL; AY135737; AAN62578.1; -
 KW Hypothetical protein.
 FT NON_TER 1
 FT NON_TER 43
 SQ SEQUENCE 43 AA; 4766 MW; 1D0A81C41F7DB35 CRC64;

Query Match 20.4%; Score 46; DB 2; Length 43;
 Best Local Similarity 33.3%; Pred. No. 1.7e+02;
 Matches 12; Conservative 10; Mismatches 10; Indels 4; Gaps 2;

QY 5 YTTDGNVTSSDGL---WNNQTQLFLEHLLTA 37
 : || : : : ||| | : : : ||| : |||
 Db 3 FVTDLSSDLNTDGLGQAW-YKISQVAVEHLLTA 37

RESULT 5

Q6WV04 PRELIMINARY; PRT; 48 AA.
 AC Q6WV04;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Defective Sdc25p (Fragment).
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RA Brachat S., Gaffney T., Philippsen P.;
 RA Lerch A., Gaffney T., Philippsen P.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RA Zhang Z., Stuart L.T., Dietrich F.S.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY268135; AAR26281.1; -
 FT NON_TER 1
 SQ SEQUENCE 48 AA; 5443 MW; EE70B5821E357BFA CRC64;

Query Match 20.2%; Score 45.5; DB 2; Length 48;
 Best Local Similarity 25.5%; Pred. No. 2.2e+02;
 Matches 12; Conservative 9; Mismatches 9; Indels 17; Gaps 2;

QY 13 VTSSDGLW-----NNQTQLFLE-----HSLLTANTTKG 42
 : || : : : ||| | : : : ||| : |||
 Db 1 LTKSGNWGDGVLIRHSANNNNNSLIDRGWPPFPFYTVHSKRTRG 47

RESULT 6

Q86LU1 PRELIMINARY; PRT; 43 AA.
 AC Q86LU1;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Cryptosporidium parvum.
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;

	Cryptosporidiidae; Cryptosporidium.
OC	NBI_TaxID=5807;
OX	[1]
RN	SEQUENCE FROM N.A.
RP	STRAIN=1876;
RC	MEDLINE=22511025; PubMed=12624019;
RX	Leoni F., Gallimore C.I., Green J., McLauchlin J.;
RA	"Molecular epidemiological analysis of Cryptosporidium isolates from humans and animals by using a heteroduplex mobility assay and nucleic acid sequencing based on a small double-stranded RNA element.";
RT	J. Clin. Microbiol. 41:981-992(2003).
RL	EMLB; AY176661; AAQ19466.1; --
RD	Hypothetical protein.
KW	FT NON TER 1
LK	FT NON TER 43
FT	NON TER 43
SQ	SEQUENCE 43 AA; 4770 MW; 130461240B2A9E35 CRC64;
	Query Match 19.6%; Score 44; DB 2; Length 43;
	Best Local Similarity 33.3%; Pred. No. 3e+02;
	Matches 12; Conservative 9; Mismatches 11; Indels 4; Gaps 2;
Oy	5 YTTDGNDTVTSSDGL---WNNTQTQLFLEHSLTLTA 37 : : : : : : : :
Dd	3 FVTDLSDFSYADLGQA-WKYISQVAVEHIILTA 37 : : : : : : : :
RESULT 7	
Q86LU6	PRELIMINARY; PRT; 43 AA.
ID Q86LU6	PRELIMINARY;
AC Q86LU6;	
DT 01-JUN-2003	(TrEMBLrel. 24, Created)
DD 01-JUN-2003	(TrEMBLrel. 24, Last sequence update)
DE 01-JUN-2003	(TrEMBLrel. 24, Last annotation update)
OS Hypothetical protein (Fragment).	
OC Cryptosporidium meleagridis.	
CC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;	
OT Cryptosporidiidae; Cryptosporidium.	
NCBI_TaxID=93969;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=1689;	
RE MEDLINE=22511025; PubMed=12624019;	
RA Leoni F., Gallimore C.I., Green J., McLauchlin J.;	
RT "Molecular epidemiological analysis of Cryptosporidium isolates from humans and animals by using a heteroduplex mobility assay and nucleic acid sequencing based on a small double-stranded RNA element.";	
RL J. Clin. Microbiol. 41:981-992(2003).	
DR EMBL; AY176647; AAQ19452.1; --	
KW Hypothetical protein.	
LK FT NON TER 1	
FT NON TER 43	
SQ SEQUENCE 43 AA; 4812 MW; FD31E1C40B323830 CRC64;	
	Query Match 19.6%; Score 44; DB 2; Length 43;
	Best Local Similarity 29.7%; Pred. No. 3e+02;
	Matches 11; Conservative 11; Mismatches 9; Indels 6; Gaps 2;
Oy	5 YTTDGNDTVTSSDGL---WNNTQTQLFLEHSLTLTA 37 : : : : : : : :
Dd	3 FVTDLSLDANTAGLGA-WKYISQTE--IEHIIMTA 37 : : : : : : : :
RESULT 8	
Q8J4I8	PRELIMINARY; PRT; 46 AA.
ID Q8J4I8	PRELIMINARY;
AC Q8J4I8;	
DT 01-OCT-2002	(TrEMBLrel. 22, Created)
DD 01-OCT-2002	(TrEMBLrel. 22, Last sequence update)
DE 01-OCT-2002	(TrEMBLrel. 22, Last annotation update)
OS Envelope glycoprotein (Fragment).	
CC Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV). viruses; Retroid viruses; Retrovridae; Lentivirus. NCBI TaxID=11723;	

Search completed: June 29, 2005, 09:46:14
Job time : 26.332 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 09:33:11 ; Search time 7.59136 Seconds
(without alignments)
413.004 Million cell updates/sec

Title: US-10-718-321-6_COPY_40_81
Perfect score: 225
Sequence: 1 PLYSYTGDNDVTSSDGL.....NNQTQLFLEHSLTANTTKG 42

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 272444

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCUTUS_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	21.3	30	4	US-09-282-029A-470
2	48	21.3	30	4	US-09-282-029A-471
3	48	21.3	30	4	US-09-434-355A-470
4	48	21.3	30	4	US-09-434-355A-471
5	45.5	20.2	40	1	US-08-188-228-22
6	45.5	20.2	40	1	US-08-332-643-22
7	45.5	20.2	40	1	US-08-332-638-22
8	44.5	19.8	31	1	US-08-190-802A-244
9	44.5	19.8	31	3	US-08-477-346-244
10	44.5	19.8	31	3	US-08-473-089-244
11	44.5	19.8	31	4	US-08-487-072A-244
12	44	19.6	20	1	US-08-218-025A-65
13	42	18.7	40	1	US-08-188-228-16
14	42	18.7	40	1	US-08-332-643-16
15	42	18.7	40	1	US-08-332-638-16
16	41.5	18.4	32	4	US-08-708-620A-4
17	41	18.2	42	4	US-09-434-355A-529
18	40	17.8	14	4	US-09-570-921-141
19	40	17.8	42	4	US-09-282-029A-6
20	40	17.8	42	4	US-09-185-908-6
21	40	17.8	42	4	US-09-434-355A-6
22	40	17.8	49	3	US-09-217-228-9
23	39.5	17.6	30	1	US-08-190-802A-123
24	39.5	17.6	30	3	US-08-477-346-123
25	39.5	17.6	30	3	US-08-473-089-123
26	39.5	17.6	30	4	US-08-487-072A-123
27	39	17.3	40	1	US-08-188-228-20

28	39	17.3	40	1	US-08-332-643-20	Sequence 20, Appl
29	39	17.3	40	1	US-08-332-638-20	Sequence 20, Appl
30	39	17.3	41	2	US-08-773-008-5	Sequence 5, Appli
31	38.5	17.1	30	1	US-08-190-802A-162	Sequence 162, App
32	38.5	17.1	30	3	US-08-477-346-162	Sequence 162, App
33	38.5	17.1	30	3	US-08-473-089-162	Sequence 162, App
34	38.5	17.1	30	4	US-08-487-072A-162	Sequence 162, App
35	38.5	17.1	31	1	US-08-190-802A-236	Sequence 236, App
36	38.5	17.1	31	3	US-08-477-346-236	Sequence 236, App
37	38.5	17.1	31	3	US-08-473-089-236	Sequence 236, App
38	38.5	17.1	31	4	US-08-487-072A-236	Sequence 236, App
39	38	16.9	21	3	US-09-252-586-18	Sequence 18, Appl
40	38	16.9	31	4	US-08-437-943D-76	Sequence 76, Appl
41	38	16.9	35	2	US-08-749-526-5	Sequence 5, Appli
42	37.5	16.7	46	4	US-08-875-553D-34	Sequence 34, Appl
43	37.5	16.7	46	4	US-08-875-553D-35	Sequence 35, Appl
44	37.5	16.7	47	3	US-08-331-625A-29	Sequence 29, Appl
45	37.5	16.7	47	3	US-09-494-151-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-09-282-029A-470
; Sequence 470, Application US/09282029A
; Patent No. 6723700
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; FILE REFERENCE: 100086.409C1
; CURRENT APPLICATION NUMBER: US/09/282, 029A
; CURRENT FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 480
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 470
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-282-029A-470

Query Match 21.3%; Score 48; DB 4; Length 30;
Best Local Similarity 45.8%; Pred. No. 10;
Matches 11; Conservative 5; Mismatches 4; Indels 4; Gaps 2;

QY 20 LWNNTQLFLEHSLTANTTKG 42
DB 2 MW---QVTAFLDHNIVTAQTWK 22

RESULT 2
US-09-282-029A-471
; Sequence 471, Application US/09282029A
; Patent No. 6723700
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; FILE REFERENCE: 100086.409C1
; CURRENT APPLICATION NUMBER: US/09/282, 029A
; CURRENT FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 480
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 471
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-282-029A-471

Query Match 21.3%; Score 48; DB 4; Length 30;

[illegible]

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,643
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US/07/872,643
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5639634and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-332-643-22

Query Match          20.2%; Score 45.5; DB 1; Length 40;
Best Local Similarity 31.7%; Pred. No. 32;
Matches 13; Conservative 5; Mismatches 8; Indels 15; Gaps 1;

QY      2 LYSYTTDGDNTVTSSDGLWNNNTQLFLEHSLLTANTTKG 42
      | : | : | : | : | : | : | : | : | : | : | : | : |
Db      2 LATAYEGNDSVAESL-----SSLESQTTEG 27

RESULT 7
US-08-332-638-22
; Sequence 22, Application US/08332638
; Patent No. 5646250
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,638
; FILING DATE: 01-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,643
; FILING DATE: 17 APR 1992
; APPLICATION NUMBER: US/08/049,460
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5646250and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-332-638-22

Query Match          20.2%; Score 45.5; DB 1; Length 40;
Best Local Similarity 31.7%; Pred. No. 32;
Matches 13; Conservative 5; Mismatches 8; Indels 15; Gaps 1;

QY      2 LYSYTTDGDNTVTSSDGLWNNNTQLFLEHSLLTANTTKG 42
      | : | : | : | : | : | : | : | : | : | : | : | : |
Db      2 LATAYEGNDSVAESL-----SSLESQTTEG 27

RESULT 8
US-08-190-802A-244
; Sequence 244, Application US/08190802A
; Patent No. 5519003
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,802A
; FILING DATE: 01-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 8600-0139
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 244:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: YCU7 r1, Fig. 48
; US-08-190-802A-244

Query Match          19.8%; Score 44.5; DB 1; Length 31;
Best Local Similarity 40.9%; Pred. No. 31;
Matches 9; Conservative 5; Mismatches 5; Indels 3; Gaps 1;

QY      4 SYTTDGDNTVTSSDGLWNNNTQLFLEHSLLTANTTKG 22
      | : | : | : | : | : | : | : | : | : | : | : | : |
Db      10 AYSPDGSRVVTASDGLKIKVWD 31

RESULT 9
US-08-477-346-244
; Sequence 244, Application US/08477346
; Patent No. 6262023
; GENERAL INFORMATION:
```

```

1 / APPLICANT: Mochly-Rosen, Daria
2 / APPLICANT: Ron, Dorit
3 / TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
4 / TITLE OF INVENTION: Thereof
5 / NUMBER OF SEQUENCES: 265
6 / CORRESPONDENCE ADDRESS:
7 / ADDRESSEE: Morrison & Foerster
8 / STREET: 2000 Pennsylvania Avenue, NW
9 / CITY: Washington
10 / STATE: DC
11 / COUNTRY: USA
12 / ZIP: 20006-1812
13 / COMPUTER READABLE FORM:
14 / MEDIUM TYPE: Floppy disk
15 / COMPUTER: IBM PC compatible
16 / OPERATING SYSTEM: PC-DOS/MS-DOS
17 / SOFTWARE: Patent in Release #1.0, Version #1.25
18 / CURRENT APPLICATION DATA:
19 / APPLICATION NUMBER: US/08/477,346
20 / FILING DATE: 07-JUN-1995
21 / CLASSIFICATION: 514
22 / PRIOR APPLICATION DATA:
23 / APPLICATION NUMBER: 08/487,072
24 / FILING DATE: 07-JUN-1995
25 / ATTORNEY/AGENT INFORMATION:
26 / NAME: MURASHIGE, KATE H.
27 / REGISTRATION NUMBER: 29,959
28 / REFERENCE/DOCKET NUMBER: 2550-0025.20
29 / TELECOMMUNICATION INFORMATION:
30 / TELEPHONE: (202) 887-1500
31 / TELEFAX: (202) 887-0763
32 / INFORMATION FOR SEQ ID NO: 244:
33 / SEQUENCE CHARACTERISTICS:
34 / LENGTH: 31 amino acids
35 / TYPE: amino acid
36 / TOPOLOGY: unknown
37 / MOLECULE TYPE: peptide
38 / HYPOTHETICAL: NO
39 / ANTI-SENSE: NO
40 / ORIGINAL SOURCE:
41 / INDIVIDUAL ISOLATE: YCU7 r1, Fig. 48
42 / US-08-477-346-244

```

Query Match 19.8%; Score 44.5; DB 3; Length 31;
Best Local Similarity 40.9%; Pred. No. 31;
Matches 9; Conservative 5; Mismatches 5; Indels 3; Gaps 1;

```
QY      4 SYTTDGN DTVT ESDG---LWN 22
        :|: |: | | | | | | | |
Db     10 AYS PDGS RVTASE PGKIKWD 31
```

RESULT 10
US-08-473-089-244
: Sequence 244. Application US/08473089

Patent No. 8342388
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```

; SOFTWARE: PatentIn Release #1.0, Version #1.2.5
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/473,089
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
;
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.22
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 244:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
;
; INDIVIDUAL ISOLATE: YCU7 rI, Fig. 48
;
; US-08-473,089-244

```

Query Match 19.8%; Score 44.5; DB 3; Length 31;
Best Local Similarity 40.9%; Pred. No. 31;
Matches 9; Conservative 5; Mismatches 5; Indels 3; Gaps 1;

```
Qy      4 SYTTDGN DTVTSSDG---LWN 22
         :|: ||: || | | | | :|:
Db     10 AYS PDGSRVVTASEDGKIKVWD 31
```

RESULT 11

```

US-08-487-072A-244
; Sequence 244, Application US/08487072A
; Patent No. 6423684
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,072A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 244:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO

```

```
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: YCU7 r1, Fig. 48
US-08-487-072A-244

Query Match      19.8%; Score 44.5; DB 4; Length 31;
Best Local Similarity 40.9%; Pred. No. 31;
Matches 9; Conservative 5; Mismatches 5; Indels 3; Gaps 1;

QY 4 SYTTDGNVTVTSSDG---LWN 22
   ||: ||: ||: ||: ||: ||:
Db 10 AVSPDGSRVVTASDGKIKVWD 31

RESULT 12
US-08-218-025A-65
; Sequence 65, Application US/08218025A
; Patent No. 5556744
; GENERAL INFORMATION:
; APPLICANT: Welner, David B.
; ADDRESSEE: Ugen, Kenneth E.
; APPLICANT: Williams, William V.
; TITLE OF INVENTION: Methods and Compositions for Diagnosing
; TITLE OF INVENTION: and Treating Certain HIV Infected Patients
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: P.O. Box 457, 321 No. 5556744tistown Road
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/218,025A
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/891,451
; FILING DATE: 29-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST33A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9206
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-218-025A-65

Query Match      19.6%; Score 44; DB 1; Length 20;
Best Local Similarity 39.1%; Pred. No. 21;
Matches 9; Conservative 4; Mismatches 2; Indels 8; Gaps 1;

QY 1 PLYSVTTDGNVTVTSSDGLWNN 23
   ||: ||: ||: ||: ||: ||:
Db 2 PLFNSTWNGNT-----WNN 16

RESULT 13
US-08-188-228-16
; Sequence 16, Application US/08188228
; Patent No. 5597725
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; CORRESPONDENCE ADDRESS:
; NUMBER OF SEQUENCES: 55
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
```

```
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,643
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/872,643
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5639634and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-332-638-16

Query Match      18.7%; Score 42; DB 1; Length 40;
Best Local Similarity 39.1%; Pred. No. 94;
Matches 9; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY      2 LYSYTTDGNVTETSSDGLMNN 24
| : | : | : | : | : | : | :
Db      2 LQTYAFEGNGSVAESLSLSDNS 24
| : | : | : | : | : | : | :

Search completed: June 29, 2005, 09:49:07
Job time : 8.59136 secs

;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-332-638-16

Query Match      18.7%; Score 42; DB 1; Length 40;
Best Local Similarity 39.1%; Pred. No. 94;
Matches 9; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY      2 LYSYTTDGNVTETSSDGLMNN 24
| : | : | : | : | : | : | :
Db      2 LQTYAFEGNGSVAESLSLSDNS 24
| : | : | : | : | : | : | :

Search completed: June 29, 2005, 09:49:07
Job time : 8.59136 secs

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,643
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/872,643
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5639634and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-332-643-16

Query Match      18.7%; Score 42; DB 1; Length 40;
Best Local Similarity 39.1%; Pred. No. 94;
Matches 9; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY      2 LYSYTTDGNVTETSSDGLMNN 24
| : | : | : | : | : | : | :
Db      2 LQTYAFEGNGSVAESLSLSDNS 24
| : | : | : | : | : | : | :

RESULT 15
US-08-332-638-16
; Sequence 16, Application US/08332638
; Patent No. 5646250
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,638
; FILING DATE: 01-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,643
; FILING DATE: 17 APR 1992
; APPLICATION NUMBER: US/08/049,460
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5646250and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
```


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OM protein - protein search, using sw model

Run on: June 29, 2005, 09:27:45 ; Search time 44.6208 Seconds
(without alignments)
720.211 Million cell updates/sec

Title: US-10-718-321-7
Perfect score: 1749
Sequence: 1 MHPQVVLILHLADSVAG.....PFKKEVQQLRPHKSCIHORE 334
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 11837

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	3.4	42	2 I70082	glycoprotein Ib al
2	56	3.2	43	2 JU0404	hypothetical 5.2K
3	55	3.1	40	2 B69408	hypothetical prote
4	53.5	3.1	46	2 S07073	arabinogalactan pr
5	50	2.9	34	2 D81044	hypothetical prote
6	49	2.8	25	2 I40692	cenA protein (lgaI
7	49	2.8	42	2 T07030	extensin - tomato
8	49	2.8	45	2 H44530	T-cell receptor al
9	48.5	2.8	27	2 A90629	thr operon leader
10	48.5	2.8	27	2 A85480	thr operon leader
11	47.5	2.7	47	2 AE3429	hypothetical prote
12	47	2.7	50	2 I38970	fibroblast growth
13	46	2.6	46	2 F81142	hypothetical prote
14	45.5	2.6	50	2 A85902	hypothetical prote
15	45	2.6	35	2 S20766	Ig heavy chain V r
16	45	2.6	47	2 B81103	hypothetical prote
17	44.5	2.5	29	2 C61384	tracheal mucin gly
18	44.5	2.5	44	2 S11110	Ig heavy chain V r
19	44.5	2.5	50	2 A82135	hypothetical prote
20	43.5	2.5	41	2 S38918	hypothetical prote
21	43.5	2.5	49	2 S49365	Ig mu chain transm
22	43	2.5	28	2 PH1363	Ig heavy chain DJ
23	43	2.5	31	2 T26228	hypothetical prote
24	43	2.5	32	2 S58524	alpha-complex prot
25	43	2.5	35	2 S30112	aminoglycoside N6'
26	43	2.5	41	2 D45495	beta-defensin-4 -
27	43	2.5	41	2 C30208	hypothetical prote
28	43	2.5	43	2 S49760	extensin - tomato
29	43	2.5	43	2 B42057	fibroblast growth

30	43	2.5	47	2 A41266	fibroblast growth
31	43	2.5	50	2 A47694	nitrate reductase
32	42.5	2.4	40	2 S33406	Ig heavy chain V r
33	42.5	2.4	43	2 A95035	hypothetical prote
34	42.5	2.4	46	2 A49281	pol protein - simi
35	42.5	2.4	49	2 S25433	neural cell adhesi
36	42	2.4	22	2 I41299	T-cell receptor be
37	42	2.4	28	2 I52394	fibronectin, splic
38	42	2.4	41	2 C87603	hypothetical prote
39	42	2.4	45	2 B46346	4.8K nonstructural
40	42	2.4	49	2 PL0096	Ig heavy chain V r
41	42	2.4	49	2 S68219	defensin AMP1 - Cl
42	42	2.4	50	2 B49410	t-complex polypept
43	41.5	2.4	36	2 A37172	collagen alpha 1(X
44	41.5	2.4	37	2 E97596	hypothetical prote
45	41.5	2.4	41	2 PQ0104	microbial serine p

ALIGNMENTS

RESULT 1

I70082 Glycoprotein Ib alpha variant B - human (fragment)

C:Species: Homo sapiens (man)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C:Accession: I70082
R:Lopez, J.A.; Ludwig, E.H.; McCarthy, B.J.
J. Biol. Chem. 267, 10055-10061, 1992
A:Title: Polymorphism of human glycoprotein Ib alpha results from a variable number of t
actions.

A:Reference number: I55355; MUID:92250564; PMID:1577776
A:Accession: I70082
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-42 <RES>
A:Cross-references: UNIPROT:Q16469; GB:S34439; NID:G249178; PID:AB22153.1; PID:G249179
C:Superfamily: platelet glycoprotein Ib alpha chain; leucine-rich alpha-2-glycoprotein r
C:Keywords: glycoprotein

Query Match 3.4%; Score 59; DB 2; Length 42;
Best Local Similarity 29.0%; Pred. No. 9.8e+02; Mismatches 15; Indels 22; Gaps 3;
Matches 18; Conservative 7;

QY	168	PRTTVPMTTMTSTTSVPTTSIPTTSVPVTTTSTVTEVPMPLEPRQNHVPATSPSSP 227
DB	2	PTSEAP-----SPTTPTSTSEAPSPPT-----PEPTSEP-APSPPTP 39
QY	228	QP 229
DB	40	EP 41

RESULT 2

JU0404

hypothetical 5.2K protein - clover yellow mosaic virus
C:Species: clover yellow mosaic virus

C>Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C:Accession: JU0404
R:Abouneidar, M.G.; Lai, R.
J. Gen. Virol. 70, 1871-1875, 1989
A:Title: Nucleotide sequence of the 3'-terminal region of clover yellow mosaic virus RNA
A:Reference number: JU0402; MUID:89293092; PMID:2738582
A:Accession: JU0404
A:Molecule type: genomic RNA
A:Residues: 1-43 <ABO>
A:Cross-references: UNIPROT:P16485; GB:D00485; NID:G221218; PID:BAA00374.1; PID:d100082

A>Note: this protein is encoded by sequence in front of the coat protein-encoding sequen

Query Match 3.2%; Score 56; DB 2; Length 43;
Best Local Similarity 40.0%; Pred. No. 1.5e+03; Mismatches 9; Indels 4; Gaps 1;
Matches 12; Conservative 5;

[illegible]

A:Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: D81044
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-34 <ET>
A:Cross-references: UNIPROT:Q9JY26; GB:AE002527; GB:AE002098; NID:g7227023; PIDN:AAF42111
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB1776

Query Match 2.9%; Score 50; DB 2; Length 34;
Best Local Similarity 37.8%; Pred. No. 2.8e+03;
Matches 14; Conservative 7; Mismatches 10; Indels 6; Gaps 2;

Qy 125 VPKVTTPIVTVPTVTTVRTSTTVPTT--TTVPTT 159
:||:||||:|:||||: :|||||:|:|
Db 1 MPWKISTTNLTVPISANL----SALPTTRCTRPPT 33

RESULT 6

I40692
cena protein (IgA1h) - Cellulomonas fimi (fragment)
C:Species: Cellulomonas fimi
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 22-Oct-1999
C:Accession: I40692
R:Miller, P.B.; Shen, H.; Gilkes, N.R.; Kilburn, D.G.; Miller, R.C.; Plaut, A.G.; Warren, FEMS Microbiol. Lett. 92, 139-204, 1992
A:Title: Endoglucanase A from Cellulomonas fimi in which the hinge sequence of human IgA1h
hoese.
A:Reference number: I40692
A:Accession: I40692
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-25 <RS>
A:Cross-references: EMBL:X65780; NID:g312035; PIDN:CAA46663.1; PID:g312036

Query Match 2.8%; Score 49; DB 2; Length 25;
Best Local Similarity 32.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 2; Mismatches 5; Indels 30; Gaps 3;

Qy 201 TTVSTFVPPMPLPRQNHPEVATSPSPQPAETHPTTLOGAIRREPTSSPLYSYTT 255
:|||||:|||||:|||||:|||||:|
Db 1 TSVST--PPTP-----SPSTP-----PTSPLOSNT 25

RESULT 7

T07030
extensin - tomato (fragment)
C:Species: Lycopersicon esculentum (tomato)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C:Accession: T07030
R:van der Eycken, W.; de Almeida Engler, J.; Inze, D.; van Montagu, M.; Cheysen, G. Plant J. 9, 45-54, 1996
A:Title: A molecular study of Meloidogyne incognita-induced feeding sites.
A:Reference number: Z15873; MUID:96158345; PMID:8580972
A:Accession: T07030
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-42 <VAN>
A:Cross-references: UNIPROT:Q40145; EMBL:Z46675; NID:G575949; PIDN:CAA86660.1; PID:G575949
A:Experimental source: strain Marmande; Meloidogyne incognita-induced root knot
C:Superfamily: hydroxyproline-rich glycoprotein
C:Keywords: cell wall; glycoprotein; hydroxyproline

C:\SpecIES\Nessleria meningitidis\Nessleria meningitidis (William Kato 2000) 09-Jul-2004
C:\Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:\Accession: D81044
R:\Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.P.A.
Hickey, E.K.; Hart, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
Li, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masiagiani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:\Authors: Brandt, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappapoli, R.; Vel

```
Query Match      2.8%; Score 49; DB 2; Length 42;
Best Local Similarity 28.6%; Pred. No. 4e+03;
Matches 14; Conservative 3; Mismatches 14; Indels 18; Gaps 2;
```

```
RESULT 8
H44530
T-cell receptor alpha chain V region (BTA27) - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000
C:Accession: H44530
R:Shiguro, N.; Tanaka, A.; Shinagawa, M.
Immunogenetics 31, 57-60, 1990
A:Title: Sequence analysis of bovine T-cell receptor alpha chain.
A:Reference number: A45893; MUID:90129157; PMID:2137108
A:Accession: H44530
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-45 <ISH>
A:Cross-references: GB:D90026; NID:G217640; PIDN:BAAL4076.1; PID:G217641
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor
F:14-23/Domain: immunoglobulin homology <IMM>

Query Match      2.8%; Score 49; DB 2; Length 45;
Best Local Similarity 31.2%; Pred. No. 4.3e+03;
Matches 10; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 85 RDVSLTIENTAVSDGVYCCVRHGWFDNM 116
   ||||| : : : : : ||| : : : : :
DB 1 RSGMSLHITASOLEDAATYLCVVDRTGVYNKL 32

RESULT 9
A90629
thr operon leader peptide [imported] - Escherichia coli (strain O157:H7, substrain RIMD
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: A90629
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11250796
A:Accession: A90629
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-27 <HAY>
A:Cross-references: UNIPROT:Q8XA85; GB:BA000007; PIDN:BA833424.1; PID:G13359457; GSPDB:G
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECS0001

Query Match      2.8%; Score 48.5; DB 2; Length 27;
Best Local Similarity 44.4%; Pred. No. 2.8e+03;
Matches 12; Conservative 4; Mismatches 4; Indels 7; Gaps 1;

QY 145 RSTTVPTTTTPTTPTTPTTMSIPTTT 171
   ||||| : : : : : ||| : : : : :
DB 3 RISTTI-----TTTITITITITT 22

RESULT 10
A85480
thr operon leader peptide [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: A85480
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A85480
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-27 <STO>
```

```
A:Cross-references: UNIPROT:Q8XA85; GB:AE005174; NID:G12512676; PIDN:AAG54301.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: thrL

Query Match      2.8%; Score 48.5; DB 2; Length 27;
Best Local Similarity 44.4%; Pred. No. 2.8e+03;
Matches 12; Conservative 4; Mismatches 4; Indels 7; Gaps 1;

QY 145 RSTTVPTTTTPTTPTTPTTMSIPTTT 171
   ||||| : : : : : ||| : : : : :
DB 3 RISTTI-----TTTITITITITT 22

RESULT 11
AE3429
hypothetical protein BME11419 [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: AE3429
R:DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, T.
; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AD3252; PMID:11756868
A:Accession: AE3429
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-47 <KUR>
A:Cross-references: UNIPROT:Q8YFV1; GB:AE008917; PIDN:AAL52600.1; PID:G17983419; GSPDB:G
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BME11419
A:Map position: 1

Query Match      2.7%; Score 47.5; DB 2; Length 47;
Best Local Similarity 45.9%; Pred. No. 5.6e+03;
Matches 17; Conservative 3; Mismatches 12; Indels 5; Gaps 3;

QY 213 PRNHEPVATSP--SSPOPAETHP-TTLQGAIRREPT 246
   ||| : : : ||| : ||| ||| ||| ||| |||
DB 12 PRR--DAVLRSPPDSAPQAPATAPNTTQNRWRELKT 46

RESULT 12
I38970
fibroblast growth factor receptor 3 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C:Accession: I38970; S52862
R:Murque, B.; Tsunekawa, S.; Rosenberg, I.; deBeaumont, M.; Podolsky, D.K.
Cancer Res. 54, 5206-5211, 1994
A:Title: Identification of a novel variant form of fibroblast growth factor receptor 3 (F
A:Reference number: I38970; MUID:95007529; PMID:7923141
A:Accession: I38970
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-50 <RES>
A:Cross-references: UNIPROT:Q8NT16; EMBL:U22410; NID:G841313; PIDN:AAA67781.1; PID:G84131
R:Scoret, E.
submitted to the EMBL Data Library, February 1995
A:Reference number: S52862
A:Accession: S52862
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-50 <SCO>
A:Cross-references: EMBL:X84939; NID:G695548; PID:G695549
C:Genetics:
A:Gene: GDB:FGFR3
A:Cross-references: GDB:127526; OMIM:100800; OMIM:134934
A:Map position: 4p16.3-4p16.3
C:Keywords: growth factor receptor
```

```
Query Match          2.7%; Score 47; DB 2; Length 50;
Best Local Similarity 45.0%; Pred. No. 6.3e+03;
Matches 9; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Qy 87 DVSLTIENTAVSDSGVCCR 106
Db 10 DVRLRLANVSERDGGEYLCLR 29

RESULT 13
F81142
hypothetical protein NMB0916 [imported] - Neisseria meningitidis (strain MC58 serogroup
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: F81142
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Va
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: F81142
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-46 <TET>
A;Cross-references: UNIPROT:Q9JZS5; GB:AE002443; GB:AE002098; NID:g7226149; PIDN:AAF4132
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB0916

Query Match          2.6%; Score 46; DB 2; Length 46;
Best Local Similarity 30.0%; Pred. No. 6.7e+03;
Matches 12; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

Qy 282 LTTANTTKGIVAGVCISVLVLLALGLGVIIAKKYPFKKEVQ 321
Db 4 LMAGVKRQIKQGGWLSVIALTSLFVSVFTLFYIFRHSVQ 43

RESULT 14
A85902
hypothetical protein Z3843 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: A85902
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A85902
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-50 <STO>
A;Cross-references: UNIPROT:Q8X447; GB:AE005174; NID:q12516979; PIDN:AGC57677.1; GSPDB:C
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z3843

Query Match          2.6%; Score 45.5; DB 2; Length 50;
Best Local Similarity 27.7%; Pred. No. 7.8e+03;
Matches 13; Conservative 5; Mismatches 18; Indels 11; Gaps 1;

Qy 35 PCHYSGAVTSMCWNRGCSLFTCQNGIVMTNGTHVYRKDTRYKLLG 81
Db 6 PIETSGVVKALVWSAALDS-----NNSHVQFQWGDVRLNGLG 41

RESULT 15
S20766
Ig heavy chain V region (VH4, IN109P1) - human (fragment)
C;Species: Homo sapiens (man)
```

C;Date: 20-Feb-1995 #sequence_revision 19-Apr-1996 #text_change 23-Jul-1999
C;Accession: S20766
R;Mortari, F.; Wang, J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A;Description: Analysis of human cord blood Ig heavy chain IgA and IgG repertoire.
A;Reference number: S20764
A;Accession: S20766
A;Molecule type: DNA
A;Residues: 1-35 <MOR>
A;Cross-references: EMBL:Z11954; NID:g33861; PIDN:CAA78011.1; PID:g33862
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 2.6%; Score 45; DB 2; Length 35;
Best Local Similarity 35.1%; Pred. No. 5.9e+03;
Matches 13; Conservative 6; Mismatches 10; Indels 8; Gaps 2;
Qy 89 SLTIENTAVSDSGVCCRVEH----RGWFNDMKITVS 121
Db 2 SVTVADTAV-----YYCARGKYGEGTRRWGQGLTVTS 34

Search completed: June 29, 2005, 09:47:29
Job time : 44.6208 secs

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OM protein - protein search, using sw model

Run on: June 29, 2005, 09:09:20 ; Search time 201.45 Seconds
(without alignments)
849.017 Million cell updates/sec

Title: US-10-718-321-7
Perfect score: 1749
Sequence: 1 MHPQVILSLHLADSVAG.....FFKKEVQQLRPHKSCIHORE 334

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 68540

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60.5	3.5	49	2 Q8J4I5	Q8J4I5 chimpanzee
2	60	3.4	47	2 Q8J4H6	Q8J4H6 chimpanzee
3	59.5	3.4	44	2 Q8J4J3	Q8J4J3 chimpanzee
4	57	3.3	48	2 Q8J193	Q8J193 chimpanzee
5	57	3.3	48	2 Q8J256	Q8J256 chimpanzee
6	56.5	3.2	39	2 Q76N72	Q76N72 mus musculus
7	56	3.2	43	1 Y5K_CXMV	P16485 clover yell
8	55.5	3.2	50	2 Q8J273	Q8J273 chimpanzee
9	55	3.1	40	1 YC67_ARCFU	O29001 archaeoglob
10	55	3.1	47	2 Q8J174	Q8J174 chimpanzee
11	55	3.1	47	2 Q8J261	Q8J261 chimpanzee
12	54	3.1	42	2 Q8E825	Q8E825 shewanella
13	54	3.1	47	2 Q8J260	Q8J260 chimpanzee
14	54	3.1	49	2 Q8BBA2	Q8BBA2 human respi
15	53.5	3.1	46	2 Q7M1G3	Q7M1G3 lolium mult
16	53.5	3.1	46	2 Q8J4I7	Q8J4I7 chimpanzee
17	53	3.0	32	2 Q76N71	Q76N71 mus musculus
18	53	3.0	45	2 Q8J315	Q8J315 chimpanzee
19	53	3.0	48	2 Q8J164	Q8J164 chimpanzee
20	53	3.0	48	2 Q8J176	Q8J176 chimpanzee
21	53	3.0	48	2 Q8J194	Q8J194 chimpanzee
22	53	3.0	48	2 Q8J201	Q8J201 chimpanzee
23	53	3.0	48	2 Q8J222	Q8J222 chimpanzee
24	53	3.0	48	2 Q8J255	Q8J255 chimpanzee
25	53	3.0	48	2 Q8J257	Q8J257 chimpanzee
26	53	3.0	48	2 Q8J258	Q8J258 chimpanzee
27	53	3.0	48	2 Q8J265	Q8J265 chimpanzee
28	53	3.0	48	2 Q8J266	Q8J266 chimpanzee
29	53	3.0	48	2 Q8J269	Q8J269 chimpanzee
30	53	3.0	49	2 Q9PXH8	Q9PXH8 chimpanzee
31	52.5	3.0	47	2 Q6QIP3	Q6QIP3 hylobates m

32	52.5	3.0	47	2 Q6QIP4	Q6QIP4 pongo pygma
33	52	3.0	47	2 Q8J4I9	Q8J4I9 chimpanzee
34	52	3.0	47	2 Q8J209	Q8J209 chimpanzee
35	52	3.0	48	2 Q8J172	Q8J172 chimpanzee
36	52	3.0	50	2 Q9PXI2	Q9PXI2 chimpanzee
37	51.5	2.9	44	2 Q9PXE2	Q9PXE2 chimpanzee
38	51.5	2.9	46	2 Q8EGR7	Q8EGR7 shewanella
39	51.5	2.9	47	2 Q6F4C0	Q6F4C0 homo sapien
40	51.5	2.9	47	2 Q6LDN6	Q6LDN6 homo sapien
41	51.5	2.9	47	2 Q6QIP5	Q6QIP5 gorilla gor
42	51.5	2.9	47	2 Q6QIP6	Q6QIP6 pan troglod
43	51.5	2.9	47	2 Q8J175	Q8J175 chimpanzee
44	51	2.9	48	2 Q8J4I6	Q8J4I6 chimpanzee
45	51	2.9	50	2 Q9E8G2	Q9E8G2 porcine ade

ALIGNMENTS

RESULT 1
Q8J4I5
ID Q8J4I5 PRELIMINARY; PRT; 49 AA.
AC Q8J4I5;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DE 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Envelope glycoprotein (Fragment).
OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11723;
RN [1]
RP SEQUENCE FROM N.A.
RA Trichel A.M., Rajakumar P.A., Murphey-Corb M.A.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY118212; AAM78572.1; -
DR GO; GO:0019031; C:viral envelope; IEA.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 49
SQ SEQUENCE 49 AA; 5101 MW; 86D35EEB15D4FC94 CRC64;

Query Match 3.5%; Score 60.5; DB 2; Length 49;
Best Local Similarity 50.0%; Pred. No. 4.5e+03;
Matches 17; Conservative 4; Mismatches 10; Indels 3; Gaps 2;
Qy 164 TMSIPTTT-TVPTTMTVSTTTSVPTTTSIPTTTS 196
Db 4 TGNVPTTATTKTITTTTSTTT--PKADVNETSS 35

RESULT 2
Q8J4H6
ID Q8J4H6 PRELIMINARY; PRT; 47 AA.
AC Q8J4H6;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DE 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Envelope glycoprotein (Fragment).
OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11723;
RN [1]
RP SEQUENCE FROM N.A.
RA Trichel A.M., Rajakumar P.A., Murphey-Corb M.A.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY118221; AAM78581.1; -
DR GO; GO:0019031; C:viral envelope; IEA.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 47
SQ SEQUENCE 47 AA; 4845 MW; EF30BF87DEF8C10B CRC64;
Query Match 3.4%; Score 60; DB 2; Length 47;


```

Qy 176 TMTVSTTTSPVPTTSTPTTSTTVPTTSTVTV 207
Db 4 TGTAKTSTASPTTTA-----SSPSTTTVTPSV 30

RESULT 9
YC67_ARCFU STANDARD; PRT; 40 AA.
AC Q29001;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hypothetical protein AF1267 precursor.
GN OrderedLocusNames=AF1267;
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RC MEDLINE=98049343; PubMed=9389475; DOI=10.1038/37052;
RA Klenk H.-P., Clayton R.A., Tomb J.-P., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M.L., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.R.,
RA Kirkness E.P., Dougherty B.A., McKenney K., Adams M.D., Loftus B.J.,
RA Peterson S.N., Reich C.I., McNeil L.K., Badger J.H., Glodek A.,
RA Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L.A.,
RA Utterback T.R., Cotton M.D., Spriggs T., Artach P., Kaine B.P.,
RA Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C.,
RA Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O.,
RA Woese C.R., Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus."
RL Nature 390:364-370(1997).
CC -----
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CC -----
DR EMBL; A3001017; AAB83992.1; -.
DR FIC; B63408; B69408.
DR TIGR; AF1267; -.
KW Complete proteome; Hypothetical protein; Signal.
FT SIGNAL 1 17 Potential.
FT CHAIN 18 40 Hypothetical protein AF1267.
FT SEQUENCE 40 AA; 4306 MW; D2535A34416EC4E6 CRC64;
SQ
Query Match 3.1%; Score 55; DB 1; Length 40;
Best Local Similarity 28.6%; Pred. No. 8.3e+03;
Matches 14; Conservative 3; Mismatches 16; Indels 16; Gaps 2;

Qy 17 SVAGSVKVGGEAGPSVTLCHYSGAVTSCWNRGSCSLFTCQNGIWTN 65
Db 2 AVAALAMYGTGCACAVLACN-----WNVREC-----GIITKN 34

RESULT 10
Q8174 PRELIMINARY; PRT; 47 AA.
AC Q8174;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Envelope-env;
GN Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
OC Chimpazee; Retrod viruses; Retroviridae; Lentivirus.

```



```
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DE 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Glycoprotein (Fragment).
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22213634; PubMed=12226836; DOI=10.1002/jmv.10225;
RA Venter M., Collinson M., Schoub B.D.;
RT "Molecular epidemiological analysis of community circulating
RT respiratory syncytial virus in rural South Africa: Comparison of
RT viruses and genotypes responsible for different disease
RT manifestations.";
RL J. Med. Virol. 68:452-461(2002).
DR EMBL; AF548809; AAN62466.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0019062; P:virion attachment; IEA.
DR InterPro; IPR000925; Glycoprot_G.
DR Pfam; PF00802; Glycoprotein_G; 1.
FT NON_TER 1
SQ SEQUENCE 49 AA; 5343 MW; DAB9CB5C890D596F CRC64;

Query Match 3.1%; Score 54; DB 2; Length 49;
Best Local Similarity 34.1%; Pred. No. 1.2e+04;
Matches 15; Conservative 4; Mismatches 25; Indels 0; Gaps 0;

QY 145 RSTSTVPTTTTPTTPTTMSIPTTTTPTTPTTMTVTTTTSVPTT 188
Db | | | | | | | | | | | | | | | | | | | |
2 RDPKTLAKTKETITNPTKPTKPTKTRDSTSTQSLVLDATTS 45

RESULT 15
Q7M1G3 PRELIMINARY; PRT; 46 AA.
AC Q7M1G3;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Arabinogalactan protein (fragments).
OS Lolium multiflorum (Italian ryegrass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Poaceae; Lolium.
OX NCBI_TaxID=4521;
RN [1]
RP SEQUENCE.
RX MEDLINE=90147544; PubMed=2695069;
RA Gleeson P.A., McNamara M., Wattenhall R.E.H., Stone B.A.,
RA Fincher G.B.;
RT "Characterization of the hydroxyproline-rich protein core of an
RT arabinogalactan-protein secreted from suspension-cultured Lolium
RT multiflorum (Italian ryegrass) endosperm cells.";
RL Biochem. J. 264:857-862(1989).
DR PIR; S07073; S07073.
FT NON_TER 1
FT NON_TER 46
SQ SEQUENCE 46 AA; 4173 MW; EF61188B0C8A08D0 CRC64;

Query Match 3.1%; Score 53.5; DB 2; Length 46;
Best Local Similarity 48.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 2; Mismatches 8; Indels 3; Gaps 1;

QY 209 FNPPLRQNHHPVA---TSPSPQPA 230
Db | | | | | | | | | | | | | | | | | | | |
16 PAPVPEASTAPVAAPTTPSPAPA 40
```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 09:27:45 ; Search time 6.94695 Seconds
(without alignments)
720.211 Million cell updates/sec

Title: US-10-718-321-7_COPY_249_300
Perfect score: 275
Sequence: 1 LYSYTTDNDVTVESSDGL.....SLLTANTTKGIYAGVCIISVL 52
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 11837

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43.5	15.8	49	2 S49365	Ig mu chain transmembrane region - bowfin
2	42.5	15.5	46	2 A49281	pol protein - simi
3	42	15.3	50	2 B49410	t-complex polypept
4	39	14.2	30	2 D82251	hypothetical prote
5	38	13.8	24	2 S00881	T-cell receptor al
6	38	13.8	35	2 S30112	aminoglycoside N6'
7	37	13.5	34	2 S68880	ribulose-bisphosph
8	37	13.5	41	2 S38918	hypothetical prote
9	37	13.5	47	2 AF0464	hypothetical prote
10	37	13.5	48	2 S29150	superoxide dismuta
11	36.5	13.3	46	2 A49281	pol protein - simi
12	36	13.1	39	2 AC0205	hypothetical prote
13	35.5	12.9	29	2 A32860	biotin-binding pro
14	35.5	12.9	33	2 I46601	myosin - pig (frag
15	35.5	12.9	33	2 I46600	myosin - pig (frag
16	35.5	12.9	37	2 AG0540	hypothetical prote
17	35	12.7	50	2 A61149	endo-1,4-beta-xyla
18	34.5	12.5	46	2 A49281	pol protein - simi
19	34.5	12.5	48	2 PL0090	Ig heavy chain v r
20	34	12.4	30	2 S70341	napin large chain
21	34	12.4	31	2 S49191	hypothetical prote
22	34	12.4	40	2 PQ0202	endo-1,4-beta-xyla
23	34	12.4	41	2 F82525	hypothetical prote
24	33.5	12.2	40	2 H95183	hypothetical prote
25	33	12.0	24	2 A36912	hypothetical prote
26	33	12.0	38	2 S72344	pili protein - Nei
27	33	12.0	41	2 C30208	hypothetical prote
28	33	12.0	48	2 AC1046	entericidin B prec
29	33	12.0	48	2 H86110	hypothetical prote

30	32.5	11.8	31	2 H82682	hypothetical prote
31	32.5	11.8	36	2 B42418	auracyanin A - Chl
32	32.5	11.8	46	2 E49281	pol protein - simi
33	32	11.6	26	2 B53113	Lys-gingipain form
34	32	11.6	28	2 G32351	34K Class B flagel
35	32	11.6	29	2 I50214	protein-cytosine-p
36	32	11.6	31	2 A57001	endo-i,4-beta-xyla
37	32	11.6	41	2 S56120	collagenase type 1
38	32	11.6	42	2 I37543	MHC HLA-DR-beta-1
39	32	11.6	45	2 D45731	gene 39.2 protein
40	32	11.6	48	2 AC1889	hypothetical prote
41	31.5	11.5	46	2 T43389	hypothetical prote
42	31	11.3	16	2 F45039	T-cell receptor be
43	31	11.3	19	2 I49422	L-lactate dehydrog
44	31	11.3	23	2 S47188	T-cell receptor J-
45	31	11.3	26	2 F45087	cysteine proteinas

ALIGNMENTS

RESULT 1

S49365

Ig mu chain transmembrane region - bowfin

C:Species: Amia calva (bowfin)

C>Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 20-Mar-1998

C:Accession: S49365

R:Wilson, M.R.; Ross, D.A.; Miller, N.W.; Clem, L.W.; Middleton, D.L.; Warr, G.W.

A:Submitted to the EMBL Data Library, October 1994

A:Description: Alternate pre-mRNA splicing pathways in the production of membrane IgM he

A:Reference number: S49365

A:Accession: S49365

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-49 <WIL>

A:Cross-references: EMBL:X82070; NID:g557218; PID:g557219

Query Match

Best Local Similarity 15.8%; Score 43.5; DB 2; Length 49;

Matches 10; Conservative 5; Mismatches 13; Indels 1; Gaps 1;

QY 2 LYSYTTDNDVTVESSDGLWNNQTLFL 30

DB 5 VFQYTVQDNG-IEYNGDSLWNTVCTFIFL 32

RESULT 2

A49281

pol protein - simian T-cell lymphotropic virus type 1, STLV-1 (isolate Bab34) (fragment)

C:Species: simian T-cell lymphotropic virus type 1, STLV-1

C>Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004

C:Accession: A49281

R:Sakaena, N.K.; Herve, V.; Durand, J.P.; Leguenno, B.; Diop, O.M.; Digoutte, J.P.; Mathi

; Paul, B.; Dube, D.K.; Barre-Sinoussi, F.; Poiesz, B.J.

Virology 198, 297-310, 1994

A:Title: Seroprevalence, molecular, and phylogenetic analyses of simian T-cell leukemia

A:Reference number: A49281; MUID:94082462; PMID:8259665

A:Accession: A49281

A:Status: preliminary; translation not shown

A:Molecule type: DNA

A:Residues: 1-46 <SAK>

A:Cross-references: UNIPROT:Q88390; GB:L20351; NID:g431689; PIDN:AAA16596.1; PID:g431690

C:Superfamily: pol polyprotein

Query Match

Best Local Similarity 15.5%; Score 42.5; DB 2; Length 46;

Matches 13; Conservative 3; Mismatches 14; Indels 3; Gaps 2;

QY 2 LYSYTTDNDVTVESSDGLWNNQTLFL 32

DB 13 LYKYTFDPLPMDNALSIGLWTFNHLNV-LTH 44


```
RESULT 8
S38918
hypotheical protein 6 - phage phi-C31
C:Species: phage phi-C31
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
R:Accession: S38918
R:Hartley, N.M.; Murphy, G.O.; Bruton, C.J.; Chater, K.P.
submitted to the EMBL Data Library, November 1993
A:Reference number: S38912
A:Accession: S38918
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-41 <HAR>
A:Cross-references: UNIPROT:Q38027; EMBL:X76288; NID:g432610; PIDN:CAA53917.1; PID:g5790
C:Genetics:
A:Start codon: GTG

Query Match 13.5%; Score 37; DB 2; Length 41;
Best Local Similarity 45.5%; Pred. No. 7.1e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 42 GYAGVCISVL 52
      |:|:|:|
DB 12 GVMVGICVGL 22

RESULT 9
AF0464
hypotheical protein YPO3815 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AF0464
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AF0464
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-47 <KUR>
A:Cross-references: UNIPROT:Q82A17; GB:AL590842; PIDN:CAC93282.1; PID:g15981729; GSPDB:G
C:Genetics:
A:Gene: YPO3815

Query Match 13.5%; Score 37; DB 2; Length 47;
Best Local Similarity 39.1%; Pred. No. 8.3e+02;
Matches 9; Conservative 5; Mismatches 7; Indels 2; Gaps 1;

QY 17 SDGLWNNQTLFLEHSLTANT 39
      ::|||:|:|:|:|:|
DB 8 NNSLGYNNVQY--HFLDSNT 28

RESULT 10
S29150
superoxide dismutase (EC 1.15.1.1) (Cu-Zn) III, cytosolic - rice (fragment)
C:Species: Oryza sativa (rice)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: S29150; B61531
R:Kanematsu, S.; Aaeda, K.
Plant Cell Physiol 31, 99-112, 1990
A:Title: Characteristic amino acid sequences of chloroplast and cytosol isozymes of CuZn
A:Reference number: S29146
A:Accession: S29150
A:Molecule type: protein
A:Residues: 1-48 <KAN>
A:Cross-references: UNIPROT:Q7M237
R:Kanematsu, S.; Aaeda, K.
Free Radic. Res. Commun. 12, 383-390, 1991
A:Title: Chloroplast and cytosol isozymes of CuZn-superoxide dismutase: their characteri
```

```
A:Reference number: A61531
A:Accession: B61531
A:Molecule type: protein
A:Residues: 1-48 <KA2>
C:Function:
A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C:Superfamily: superoxide dismutase (Cu-Zn)
C:Keywords: copper; cytosol; metalloprotein; oxidoreductase; zinc
F:44.46/Binding site: copper (His) #status predicted

Query Match 13.5%; Score 37; DB 2; Length 48;
Best Local Similarity 50.0%; Pred. No. 8.5e+02;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 3 YSYTTDGNQDVTVTSSDGL 20
      :|:|:|:|:|
DB 19 FSQEGDGPTTXXSVSGL 36

RESULT 11
F49281
pol protein - simian T-cell lymphotropic virus type 1, STLV-1 (fragment)
C:Species: simian T-cell lymphotropic virus type 1, STLV-1
C>Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004
C:Accession: F49281; B49281
R:Saksena, N.K.; Herve, V.; Durand, J.P.; Leguennou, B.; Diop, O.M.; Digoutte, J.P.; Mathi
; Paul, B.; Dube, D.K.; Barre-Sinoussi, P.; Poiesz, B.J.
Virology 198, 297-310, 1994
A:Title: Seroepidemiologic, molecular, and phylogenetic analyses of simian T-cell leukemia
A:Reference number: A49281; MUID:94082462; PMID:8259665
A:Accession: F49281
A>Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-46 <SAK>
A:Cross-references: UNIPROT:Q88344; UNIPROT:Q88360; UNIPROT:Q88343; UNIPROT:Q88394; UNIP
PROT:Q88331; UNIPROT:Q88406; GB:I20357; NID:9431721; PIDN:AAA16561.1; PID:g431722
A:Experimental source: isolate SAB37Pol
A:Accession: B49281
A>Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-46 <SA2>
A:Cross-references: GB:L20358; NID:9431709; PIDN:AAA16556.1; PID:g431710
A:Experimental source: isolate SAB91037
C:Superfamily: pol polyprotein

Query Match 13.3%; Score 36.5; DB 2; Length 46;
Best Local Similarity 36.4%; Pred. No. 9.3e+02;
Matches 12; Conservative 3; Mismatches 15; Indels 3; Gaps 2;

QY 2 LYSYTTDGNQDVTVTSS--SDGLWNNNQTLFLEH 32
      |||:|:|:|:|:|
DB 13 LYKYFTDKPDLPMDNALSIALWTINHLNV-LTH 44

RESULT 12
AC0205
hypotheical protein YPO1682 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AC0205
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AC0205
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-39 <KUR>
A:Cross-references: UNIPROT:Q8ZF17; GB:AL590842; PIDN:CAC90503.1; PID:g15979714; GSPDB:G
C:Genetics:
A:Gene: YPO1682
```

A;Residues: 1-33 <BEM>
A;Cross-references: UNIPROT:Q29066; GB:L29135; NID:ig457345; PIDN:AAA20920.1; PID:g5311151
C;Superfamily: myosin heavy chain 95F; myosin motor domain homology

Query Match	12.9%;	Score 35.5;	DB 2;	Length 33;
Best Local Similarity	47.8%;	Pred. No. 8.4e+02;		
Matches 11;	Conservative 3;	Mismatches 8;	Indels 1;	Gaps 1;

Qy 25 QTQLFLEHSLTLTANTTKGIYAGV 47
| : | | | | : | |
| : | | | | : | |
Db 1 QSTNFIHH-LTALSQKFSAGV 22

Search completed: June 29, 2005, 09:47:30
Job time : 7.94695 secs

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Query Match          13.1%; Score 36; DB 2; Length 39;
Best Local Similarity 32.0%; Pred.No. 8.9e+02;
Matches      8; Conservative    4; Mismatches   13; Indels    0; Gaps    0;

QY      23 NNQTQLFLEHSLLTANTTKGIYAGV 47
       :|: | : | | | | | | | |
DB      11 DNRKLLADGIKSTVTNKGVIYIAV 35

RESULT 13
A32860
biotin-binding protein I - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change 24-Jun-1993
C;Accession: A32860
R;Bush, L.; White III, H.B.
J. Biol. Chem. 264, 5741-5745, 1989
A;Title: Conversion of domains into subunits in the processing of egg yolk biotin-binding
A;Reference number: A32860; MUID:89174629; PMID:2925632
A;Accession: A32860
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-29 <BUS>
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```

Query Match          12.9%; Score 35.5; DB 2; Length 29;
Best Local Similarity 52.9%; Pred. No. 7.3e+02;
Matches 9; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

QY      19 GLANNNOTLPLEHSL 35
      ||||| :|||
Db       9 GLWENEQDSL-MEISAL 24

RESULT 14
I46501
myosin - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C:Accession: I46601
R:Bement, W.M.; Hasson, T.; Wirth, J.A.; Cheney, R.E.; Mooseker, M.S.
Proc. Natl. Acad. Sci. U.S.A. 91, 6549-6553, 1994
A:Title: Identification and overlapping expression of multiple unconventional myosin genes
A:Reference number: A55758; MUID:94294418; PMID:8022818
A:Accession: I46601
A:Status: preliminary; translated from GB/EMBL/DBDB
A:Molecule type: mRNA
A:Residues: 1-33 <BEN>
A:Cross-references: UNIPROT:Q29067; GB:L29136; NID:G457346; PIDN:AAA20921.1; PID:G531152
C:Superfamily: myosin heavy chain 95F; myosin motor domain homology

```

```

Query Match      12.9%; Score 35.5; DB 2; Length 33;
Best Local Similarity 42.9%; Pred.No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

Qy    25 QTQLFLEHSLTANTTKGIYAGVCISVL 52
       |:|:|||||:||||:|::|:|
Db     1 QSTNFLIH-CLITALSQKGYSAGVERTIL 27

RESULT 15
I46600
myosin - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C:Accession: I46600
R:Bement, W.M.; Hasson, T.; Wirth, J.A.; Cheney, R.E.; Mooseker, M.S.
Proc. Natl. Acad. Sci. U.S.A. 91, 6549-6553, 1994
A:Title: Identification and overlapping expression of multiple unconventional myosin genes
A:Reference number: A55758; MUID:94294418; PMID:8022818
A:Accession: I46600
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
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Result No.	Score	Query %		DB	Length	ID	Description
		Match	Length				
1	47	17.1	43	2	Q86LU3	2	Q86LU3 cryptospori
2	46	16.7	43	2	Q81OR6	6	Q81OR6 cryptospori
3	46	16.7	43	2	Q81OR7	7	Q81OR7 cryptospori
4	46	16.7	43	2	Q81SB4	4	Q81SB4 saccharomyc
5	45.5	16.5	48	2	Q6WV04	2	Q6WV04 saccharomyc
6	44	16.0	43	2	Q86LU1	4	Q86LU1 cryptospori
7	44	16.0	43	2	Q86LU6	6	Q86LU6 cryptospori
8	44	16.0	46	2	Q8J4I8	8	Q8J4I8 chimpanzee
9	44	16.0	49	2	Q8J4I5	5	Q8J4I5 chimpanzee
10	43.5	15.8	41	2	Q99JT4	4	Q99JT4 mus musculu
11	43	15.6	41	2	Q7RDL1	1	Q7RDL1 plasmodium
12	43	15.6	43	2	Q86LU2	2	Q86LU2 cryptospori
13	43	15.6	43	2	Q86LU5	5	Q86LU5 cryptospori
14	42.5	15.5	46	2	Q88390	0	Q88390 simian t-ly
15	42	15.3	43	2	Q86LU4	4	Q86LU4 cryptospori
16	42	15.3	46	2	Q7KYS6	6	Q7KYS6 homo sapien
17	42	15.3	47	2	Q8J4I9	9	Q8J4I9 chimpanzee
18	41.5	15.1	47	2	Q75JX4	4	Q75JX4 dictyosteli
19	41	14.9	29	2	Q86233	3	Q86233 human rotav
20	41	14.9	40	2	Q83DR8	8	Q83DR8 coxiella bu
21	41	14.9	41	2	O11552	2	O11552 human immun
22	40.5	14.7	49	2	Q91FZ1	1	Q91FZ1 chilo iride
23	40	14.5	49	2	Q7XA54	4	Q7XA54 gnetum gnem
24	39.5	14.4	46	2	Q82209	9	Q82209 human t-lym
25	39.5	14.4	47	2	Q89Z69	7	Q89Z69 leptospira
26	39	14.2	28	2	Q998S5	5	Q998S5 turkey ente
27	39	14.2	30	2	Q9XT75	5	Q9XT75 vibrio chol
28	39	14.2	35	2	Q6QPN9	9	Q6QPN9 human immun
29	39	14.2	38	2	Q7RD73	3	Q7RD73 plasmodium
30	39	14.2	47	2	Q65SH0	4	Q65SH0 manneimia
31	39	14.2	50	2	Q7SEZ1	1	Q7SEZ1 neurospora

Db 3 FVTDLSDDLNTADGLQAW-YKISQAEIEHIMTA 37

Search completed: June 29, 2005, 09:46:16
Job time : 32.3635 secs

Db 3 FVTDLSSDLNTADGLQAW-YKISQVEVEHIIMTA 37

RESULT 14	Q88390	PRELIMINARY;	PRT; 46 AA.
ID	Q88390	PRELIMINARY;	PRT; 46 AA.
AC	Q88390;		
DT	01-NOV-1996	(T-EMBLrel. 01, Created)	
DT	01-NOV-1996	(T-EMBLrel. 01, Last sequence update)	
DT	01-JUN-2003	(T-EMBLrel. 24, Last annotation update)	
DE	Pol protein (Fragment).		
GN	Name=pol;		
OS	Simian T-lymphotropic virus 1.		
OC	Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.		
OX	NCBI_TaxID=33747;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=94082462; PubMed=8259665;		
RA	Saksena N.K., Herve V., Durand J.P., LeGuennou B., Diop O.M.,		
RA	Digoutte J.P., Mathiot C., Muller M.C., Love J.L., Benz P.M.,		
RA	Erceyoy S., Barre-Sinoussi F., Poiesz B.J.;		
RT	"seroepidemiologic, molecular, and phylogenetic analyses of simian T-		
RT	cell leukemia viruses (STLV-I) from various naturally infected monkey		
RL	species from central and western Africa.";		
RL	Virology 198:297-310(1994).		
DR	EMBL: L20351; AAA16596.1; -.		
DR	PIR: A49281; A49281.		
FT	NON_TER 1		
FT	NON_TER 46		
SQ	SEQUENCE 46 AA; 5357 MW; 7416828B6E7330E51 CRC64;		

Query Match 15.5%; Score 42.5; DB 2; Length 46;
Best Local Similarity 39.4%; Pred. No. 9.5e+02;
Matches 13; Conservative 3; Mismatches 14; Indels 3; Gaps 2;

QY 2 LYSYTTDGNIVTES--SDGLWNNQTQLFLEH 32
||| ||| :: ||| : |||
Db 13 LKYEFTDKPDPMPMDNALSIGLWTFNHLNV-LTH 44

RESULT 15					
ID	Q86LU4	PRELIMINARY;	PRT;	43 AA.	
DC	Q86LU4;				
AT	01-JUN-2003	(TrEMBLrel. 24, Created)			
DT	01-JUN-2003	(TrEMBLrel. 24, Last sequence update)			
DI	01-JUN-2003	(TrEMBLrel. 24, Last annotation update)			
DE	Hypothetical protein (Fragment).				
OS	Cryptosporidium felis.				
OC	Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;				
OC	Cryptosporidiidae; Cryptosporidium.				
NCBI_TaxID=83540;					
RX	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=1626;				
RX	MEDLINE=22511025; PubMed=12624019;				
RT	leoni F., Gallimore C.I., Green J., McLauchlin J.;				
RT	"Molecular epidemiological analysis of Cryptosporidium isolates from				
RT	humans and animals by using a heteroduplex mobility assay and nucleic				
RT	acid sequencing based on a small double-stranded RNA element.";				
J. Clin. Microbiol. 41:981-992(2003)."					
RL	EMBL; AY176651; AAO19456.1; -.				
KW	Hypothetical protein.				
FT	NON TER	1			
FT	NON TER	43			
SQ	SEQUENCE	43 AA;	4798 MW;	CBIF81C40B323833 CRC64;	
Query Match		15.3%;	Score 42;	DB 2;	Length 43;
Best Local Similarity		30.6%;	Pred. No. 1e+03;		
Matches	11;	Conservative	10;	Mismatches	11;
				Indels	4;
				Gaps	

QY 5 YTTDGN DTVTSSDGL---WNNNQTLFLEHSLTA 37

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 08:57:16 ; Search time 36.9823 Seconds
(without alignments)

543.815 Million cell updates/sec

Title: US-10-718-321-7_COPY_249_300

Perfect score: 275

Sequence: 1 PLYSVTTDGNDRVTSSDGL.....SLLTANTYKGIYGVICISVL 52

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	275	100.0	334	2	Aaw38336 Human kid
2	275	100.0	334	6	Aao26679 KIM-1 rel
3	275	100.0	334	8	Adq76696 Human kid
4	275	100.0	339	7	Adq36618 Plasmid p
5	275	100.0	339	7	Adq36592 Human NOV
6	275	100.0	359	6	Adr58582 Human can
7	275	100.0	359	6	Abp70439 Amino aci
8	275	100.0	359	6	Abp70438 Amino aci
9	275	100.0	359	6	Abp70437 Amino aci
10	275	100.0	359	6	Abp70436 Amino aci
11	275	100.0	359	7	Adq36594 Human NOV
12	275	100.0	359	7	Adn38984 Cancer/an
13	275	100.0	359	8	Adq76690 Human kid
14	275	100.0	364	6	Abp70442 Amino aci
15	275	100.0	365	6	Abp70440 Amino aci
16	270	98.2	359	6	Abp70441 Amino aci
17	270	98.2	364	6	Abp70443 Amino aci
18	228	82.9	298	8	Adq76693 Human KIM
19	228	82.9	451	2	AAK92803 Hepatitis
20	228	82.9	518	8	Adq76691 Human KIM
21	225	81.8	81	6	Aao26678 Human KIM
22	189	68.7	263	7	Adq36629 Human NOV
23	189	68.7	263	7	Adq36622 Plasmid p
24	189	68.7	263	7	Adq36596 Human NOV
25	101	36.7	18	6	Aao26686 Human KIM

26	99	36.0	18	6	AAO26687	Aao26687 Human KIM
27	99	36.0	18	6	AAO26673	Aao26673 Monoclonal
28	90	32.7	18	6	AAO26688	Aao26688 Human KIM
29	82	29.8	18	6	AAO26685	Aao26685 Human KIM
30	79	28.7	305	6	ABP70430	Amino aci
31	78	28.4	307	2	AAW38334	Rat kidne
32	76.5	27.8	282	6	ABP70431	Amino aci
33	62.5	22.7	774	8	ADG93320	ADG93320 DEN1 (Pue
34	62.5	22.7	775	8	ADG93318	ADG93318 DEN1 (Pue
35	62	22.5	606	4	AAW78898	C. glutam
36	60.5	22.0	474	5	ABO4708	Human SP1
37	60.5	22.0	474	6	ABU00247	Human nov
38	60.5	22.0	474	7	ADG31674	Human pro
39	60	21.8	219	3	AAW38336	AAW38336 standard; protein; 334 AA.
40	60	21.8	249	3	AAW38336	AAW38336; Human kidney injury related molecule (KIM).
41	60	21.8	249	3	AAW38336	Human kidney injury related molecule (KIM).
42	60	21.8	268	3	AAW38336	Kidney injury related molecule; KIM; human; renal disease; injury; nephritis; tissue regeneration; therapy; monoclonal antibody.
43	60	21.8	268	3	AAW38336	Kidney injury related molecule; KIM; human; renal disease; injury; nephritis; tissue regeneration; therapy; monoclonal antibody.
44	60	21.8	338	3	AAW38336	Kidney injury related molecule; KIM; human; renal disease; injury; nephritis; tissue regeneration; therapy; monoclonal antibody.
45	60	21.8	338	8	AAW38336	Kidney injury related molecule; KIM; human; renal disease; injury; nephritis; tissue regeneration; therapy; monoclonal antibody.

ALIGNMENTS

RESULT 1

AAW38336

ID AAW38336 standard; protein; 334 AA.

XX AAW38336;

XX DT 21-MAY-1998 (first entry)

XX DE Human kidney injury related molecule (KIM).

XX KW Kidney injury related molecule; KIM; human; renal disease; injury; nephritis; tissue regeneration; therapy; monoclonal antibody.

XX OS Homo sapiens.

XX PN WO744460-A1.

XX PD 27-NOV-1997.

XX PF 23-MAY-1997; 97WO-US009303.

XX PR 24-MAY-1996; 96US-0018228P.

XX PR 23-AUG-1996; 96US-0023442P.

XX (BIOJ) BIOGEN INC.

XX Sanicola-Nadel M, Bonventre JV, Hession CA, Ichimura T, Wei H; Cate RL;

XX WPI; 1998-018514/02.

XX DNA encoding kidney injury related molecule - which is upregulated in injured or regenerating tissue, useful to promote growth of new tissue and survival of damaged tissue.

XX Claim 9; Page 46-47; 68pp; English.

This protein, designated kidney injury related molecule (KIM), is up-regulated in injured or regenerating tissue. Its amino acid sequence was deduced from a clone (see AAW38336) obtained from a human embryonic liver library. A 578-amino acid (see AAW38336) and a 307-amino acid rat KIM (see AAW38334) are also claimed. Recombinant KIM polypeptides can be expressed in prokaryotic and eukaryotic host cells using a claimed process. Soluble variants fused to a toxin, imageable compound or radionuclide, and IgG fusion proteins are also claimed. KIM, or an agonist, can be used to treat renal disease and to promote the growth of new tissue or the survival of damaged tissue, generally in conditions where the binding of specific ligand to KIM stimulates cell growth, maintains

CC cellular differentiation or reduces apoptosis, e.g. in cases of renal
CC failure, nephritis, kidney transplants, toxic or hypoxic injury. A
CC monoclonal antibody specific for KIM can be used to treat renal disease,
CC e.g. where binding of KIM to ligand results in neoplasia, loss of
CC cellular function, susceptibility to apoptosis or promotion of
CC inflammation, deliver imaging agents to KIM expressing cells in vivo or
CC in vitro and measure KIM concentration by immunoassay.
CC Damage/regeneration of renal cells can be determined by measuring KIM,
CC particularly to diagnose or monitor the progress of disease or therapy.
CC KIM-expressing tumour cells can be inhibited by treatment with a fusion
CC protein comprising KIM ligand or MAb with a toxin or radionuclide, and
CC tumour cells that express KIM ligand can be inhibited with similarly
CC tagged KIM or anti-KIM ligand antibody
XX
SQ Sequence 334 AA;

Query Match 100.0%; Score 275; DB 2; Length 334;
Best Local Similarity 100.0%; Pred. No. 7.3e-26;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLYSVTTDGNQDVTVESSDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 52
|||||
DB 249 PLYSVTTDGNQDVTVESSDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 300

RESULT 2
AAO26679
ID AAO26679 standard; protein; 334 AA.

AC AAO26679;
DT 20-MAR-2003 (first entry)
XX
DE KIM-1 related protein, SEQ ID No 7.
XX
KW Cytostatic; gene therapy; antibody; antigen; antigen-binding;
KW proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;
KW renal disease; injury; renal cancer; human.

OS Homo sapiens.

XX WO200298920-A1.

PN 12-DEC-2002.

PD 31-MAY-2002; 2002WO-US017402.

PF 01-JUN-2001; 2001US-0295449P.

PR 04-JUN-2001; 2001US-0295907P.

XX (BIOJ) BIOGEN INC.

PA (GENO) GEN HOSPITAL CORP.

XX Bailly V, Bonventre J;

XX WPI; 2003-156845/15.

XX New antibody, antibody derivative or antigen-binding polypeptide that
PT inhibits proteolytic release of a soluble kidney injury molecule-1
PT polypeptide, useful for treating or preventing renal disease or injury,
PT e.g. renal cancer.

XX Disclosure; Page 39-40; 42pp; English.

XX The invention relates to a novel antibody, antibody derivative or antigen
CC -binding polypeptide that inhibits proteolytic release of a soluble
CC kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.
CC The antibody, antibody derivative or antigen-binding polypeptide is
CC useful for treating or preventing renal disease or injury, e.g. renal
CC cancer. The antibody is also useful for inhibiting shedding of the KIM-1
CC polypeptide. This sequence represents a protein relating to the KIM-1
CC protein of the invention

SQ Sequence 334 AA;

Query Match 100.0%; Score 275; DB 6; Length 334;
Best Local Similarity 100.0%; Pred. No. 7.3e-26;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLYSVTTDGNQDVTVESSDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 52
|||||
DB 249 PLYSVTTDGNQDVTVESSDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 300

RESULT 3

ID ADO76696 standard; protein; 334 AA.

XX ADO76696;

DT 16-DEC-2004 (first entry)

XX Human kidney injury molecule-1 (KIM-1).

XX Human; KIM-1; kidney injury molecule-1; immunosuppressive; protozoacide;
KW muscular-gen.; neuroprotective; antianaemic; antithyroid; haemostatic;
KW antiallergic; antiinflammatory; vasotropic; nephropic.

OS Homo sapiens.

FH Key Location/Qualifiers
FT Peptide 1..20
FT /label= Signal_peptide

FT Modified-site 65..67
FT /note= "N-glycosylated"

FT Modified-site 258..260
FT /note= "N-glycosylated"

FT Modified-site 272..274
FT /note= "N-glycosylated"

FT Modified-site 286..288
FT /note= "N-glycosylated"

FT Domain 290..311
FT /note= "Transmembrane domain"

FT Region 324..334

FT /note= "C-terminal region unique to this splice variant"

XX WO2004060041-A2.

XX 22-JUL-2004.

XX 29-DEC-2003; 2003WO-US041294.

XX 30-DEC-2002; 2002US-0436934P.

XX (BIOG-) BIOGEN IDEC MA INC.

XX Rennert PD;

XX WPI; 2004-534277/51.

XX Use of a kidney injury molecule-1 (KIM-1) antagonist for e.g. treating
PT Th2 cell-mediated diseases or inflammatory diseases, inhibiting B cell
PT activation, or inhibiting production of a subset of antibodies against
PT one or more antigens.

XX Disclosure; SEQ ID NO 1; 68pp; English.

XX The present sequence is that of human kidney injury molecule-1 (KIM-1), a
CC type I cell membrane glycoprotein and member of the T cell immunoglobulin
CC (Ig) and mucin domain (TIM) family. This protein has 334 amino acids or
CC 359 amino acids ADO76690, depending on splice variation. It has been
CC discovered that treatment of a mammal with a KIM-1 antagonist alters the
CC interaction of T cells and other immune system cells, e.g. dendritic
CC cells, monocytes, macrophages and B cells, and thereby strongly
CC suppresses an IgG response to an antigen. Such treatment also eliminates
CC IgG1 production by memory B cells in response to subsequent challenge

PT New polypeptide, useful for preparing a composition for treating or

The present invention describes an isolated human NOVX polypeptide, where x is 1a to 1d or 2a to 2h, or its mature form, a sequence that is at least 95 % identical to it, or a sequence comprising one or more conservative substitutions in the amino acid sequence. The NOVX polypeptide, and nucleic acid sequence encoding it, has cytostatic and antiinflammatory activities, and can be used in gene therapy, and in vaccines. The NOVX polypeptide is useful for preparing a composition for

CC treating or preventing a pathology associated with NOVX polypeptide e.g.
CC renal cancer or inflammation, or for tissue typing. The present sequence
CC represents human NOV1a from the present invention.

XX
SQ Sequence 339 AA;

Query Match 100.0%; Score 275; DB 7; Length 339;
Best Local Similarity 100.0%; Pred. No. 7.5e-26;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLYSYTTDGNVTVTSSDGLWNNNTQLFLEHSLLTANTTKGIYAGVCISVL 52
|||||
Db 229 PLYSYTTDGNVTVTSSDGLWNNNTQLFLEHSLLTANTTKGIYAGVCISVL 280
|||||

RESULT 6

ABR58582
ID ABR58582 standard; protein; 359 AA.

XX ABR58582;

XX 09-JUL-2003 (first entry)

DT Human cancer related protein SEQ ID NO:239.

DE Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
KW heart disease; atherosclerosis; endometriosis.

XX Homo sapiens.

XX WO2003025138-A2.

XX 27-MAR-2003.

XX 17-SEP-2002; 2002WO-US029560.

XX 17-SEP-2001; 2001US-0323469P.

XX 20-SEP-2001; 2001US-0323887P.

XX 13-NOV-2001; 2001US-0350668P.

XX 08-FEB-2002; 2002US-0355145P.

XX 08-FEB-2002; 2002US-0355257P.

XX 12-APR-2002; 2002US-0372246P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KB;

PI Zlotnik A;

XX WPI; 2003-354600/33.

XX N-PSDB; ACC72709.

XX New genes that are up-regulated or down-regulated in cancers, useful as
PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
PT therapeutic targets for screening drugs for treating these diseases.

XX Claim 12; Page 742; 767pp; English.

XX The present invention describes an isolated nucleic acid molecule, which
CC comprises the sequence of any of the genes that are up-regulated or down-
CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
CC related gene nucleotide sequences which encode the proteins given in
CC ABR58582 to ABR58709. Also described: (1) determining the presence or
CC absence of a pathological cell in a patient; (2) an expression vector
CC comprising a nucleic acid molecule described above; (3) a host cell
CC comprising the vector; (4) an isolated polypeptide, which is encoded by
CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
CC of (4); (6) specifically targeting a compound to a pathological cell in a
CC patient by administering to the patient the antibody above; and (7) a
CC drug screening assay. The nucleic acid is useful as diagnostic markers or
CC therapeutic targets. In particular, the nucleic acid is useful for
CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,

CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
CC atherosclerosis and endometriosis. The nucleic acid is also useful in
CC drug screening, particularly for identifying agents for treating these
CC pathologies

XX SQ Sequence 359 AA;

Query Match 100.0%; Score 275; DB 6; Length 359;
Best Local Similarity 100.0%; Pred. No. 8e-26;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLYSYTTDGNVTVTSSDGLWNNNTQLFLEHSLLTANTTKGIYAGVCISVL 52
|||||
Db 249 PLYSYTTDGNVTVTSSDGLWNNNTQLFLEHSLLTANTTKGIYAGVCISVL 300
|||||

RESULT 7

ABP70439

ID ABP70439 standard; protein; 359 AA.

XX ABP70439;

XX 22-APR-2003 (first entry)

DE Amino acid sequence of human TIM-1 allele 1.

XX T cell immunoglobulin domain; mucin domain; TIM; TIM-1; TIM-2; TIM-3;
KW TIM-4; immune dysfunction; chromosome 5; malignancy; allergy; eczema;
KW myelodysplastic syndrome; airway hyperreactivity; cancer; asthma;
KW allergic T cell response; autoimmune disease.

XX Homo sapiens.

XX WO2003002722-A2.

XX 09-JAN-2003.

XX 01-JUL-2002; 2002WO-US020890.

XX 29-JUN-2001; 2001US-0302344P.

XX (STRD) UNIV LELAND STANFORD JUNIOR.

XX McIntire JJ, Dekrueff RH, Umetsu DT, Freeman GJ, Kuchroo V;

XX WPI; 2003-210268/20.

XX N-PSDB; ABZ68333.

XX New nucleic acid comprising a mammalian T cell immunoglobulin domain and
PT Mucin domain gene sequences, useful for treating cancer or asthma,
PT allergy, eczema or autoimmune disease.

XX Claim 10; Page 82; 94pp; English.

XX The present sequence is a human T cell immunoglobulin domain and mucin
CC domain-1 (TIM-1) polypeptide. The specification describes TIM-1, TIM-2,
CC TIM-3 and TIM-4. TIM polypeptides are cell surface molecules with
CC conserved IgV and mucin domains. The locus comprising the TIM family is
CC genetically associated with immune dysfunction, including asthma. The TIM
CC gene family is located within a region of human chromosome 5 that is
CC commonly deleted in malignancies and myelodysplastic syndrome. Variants
CC of TIM-1 and TIM-3 are associated with susceptibility to airway
CC hyperreactivity and allergic T cell responses, and other variants
CC associated with protection against these responses. T cells express TIM
CC proteins, which critically regulate CD4 T cell differentiation. Th1 cells
CC preferentially express TIM-3, while Th2 cells preferentially express TIM-
CC 1. TIM polypeptides and polynucleotides are useful for treating cancer,
CC asthma, allergies, eczema or autoimmune diseases

XX SQ Sequence 359 AA;

Query Match 100.0%; Score 275; DB 6; Length 359;
Best Local Similarity 100.0%; Pred. No. 8e-26;

Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLYSYTTDGNVTSSDGLWNNNTQLFLEHSLLTANTTKGIYAGVCISVL 52
|||||
Db 249 PLYSYTTDGNVTSSDGLWNNNTQLFLEHSLLTANTTKGIYAGVCISVL 300

RESULT 8
ABP70438
ID ABP70438 standard; protein; 359 AA.
AC ABP70438;
XX
XX
DT 22-APR-2003 (first entry)
XX
XX
DE Amino acid sequence of human TIM-1 allele 1.
XX
XX
KW T cell immunoglobulin domain; mucin domain; TIM; TIM-1; TIM-2; TIM-3;
KW TIM-4; immune dysfunction; chromosome 5; malignancy; allergy; eczema;
KW myelodysplastic syndrome; airway hyperreactivity; cancer; asthma;
KW allergic T cell response; autoimmune disease.
XX
OS Homo sapiens.
XX
XX WO2003002722-A2.
PN
XX
XX 09-JAN-2003.
PD
PF 01-JUL-2002; 2002WO-US020890.
XX
XX 29-JUN-2001; 2001US-0302344P.
PR
XX (STRD) UNIV LELAND STANFORD JUNIOR.
PA
XX
PI McIntire JJ, Dekruff RH, Umetsu DT, Freeman GJ, Kuchroo V;
XX
XX WPI; 2003-210268/20.
DR
DR N-PSDB; ABZ68332.
XX
XX New nucleic acid comprising a mammalian T cell immunoglobulin domain and
PT Mucin domain gene sequences, useful for treating cancer or asthma,
PT allergy, eczema or autoimmune disease.
XX
XX Claim 10; Page 80-81; 94pp; English.
PS
XX The present sequence is a human T cell immunoglobulin domain and mucin
CC domain-1 (TIM-1) polypeptide. The specification describes TIM-1, TIM-2,
CC TIM-3 and TIM-4. TIM polypeptides are cell surface molecules with
CC conserved IgV and mucin domains. The locus comprising the TIM family is
CC genetically associated with immune dysfunction, including asthma. The TIM
CC gene family is located within a region of human chromosome 5 that is
CC commonly deleted in malignancies and myelodysplastic syndrome. Variants
CC of TIM-1 and TIM-3 are associated with susceptibility to airway
CC hyperactivity and allergic T cell responses, and other variants
CC associated with protection against these responses. T cells express TIM
CC proteins, which critically regulate CD4 T cell differentiation. Th1 cells
CC preferentially express TIM-3, while Th2 cells preferentially express TIM-
CC 1. TIM polypeptides and polynucleotides are useful for treating cancer,
CC asthma, allergies, eczema or autoimmune diseases
XX
SQ Sequence 359 AA;

Query Match 100.0%; Score 275; DB 6; Length 359;
Best Local Similarity 100.0%; Pred. No. 8e-26;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLYSYTTDGNVTSSDGLWNNNTQLFLEHSLLTANTTKGIYAGVCISVL 52
|||||
Db 249 PLYSYTTDGNVTSSDGLWNNNTQLFLEHSLLTANTTKGIYAGVCISVL 300

RESULT 9
ABR48174
ID ABR48174 standard; protein; 359 AA.
AC ABR48174;
XX
XX
DT 12-JUN-2003 (first entry)
XX
XX
DE Human bladder cancer associated protein sequence SEQ ID NO:64.
KW Human; bladder cancer; cytostatic; gene therapy; vaccine.
OS Homo sapiens.
XX
XX WO2003003906-A2.
PN
XX
XX 16-JAN-2003.
PD
PF 03-JUL-2002; 2002WO-US021338.
XX
XX 03-JUL-2001; 2001US-0302814P.
PR
XX 03-AUG-2001; 2001US-0310099P.
PR
XX 08-NOV-2001; 2001US-0343705P.
PR
XX 13-NOV-2001; 2001US-0350666P.
PR
XX 12-APR-2002; 2002US-0372246P.
PR
XX (EOSE-) EOS BIOTECHNOLOGY INC.
PA
XX
XX Mack DH, Aziz N;
PI
XX
XX WPI; 2003-201532/19.
DR
DR N-PSDB; ACC50985.
XX
XX Detecting a bladder cancer-associated transcript in a cell from a
PT patient, comprises contacting a biological sample from the patient with a
PT bladder cancer-associated polynucleotide or antibody.
XX
XX Claim 10; Page 252; 307pp; English.
PS
XX The present invention describes a method for detecting a bladder cancer-
CC associated transcript in a cell from a patient. The method comprises
CC contacting a biological sample from the patient with a polynucleotide
CC that selectively hybridizes to a sequence that is 80 % identical to a
CC table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059
CC encode the human bladder cancer-associated proteins given in ABR48146 to
CC ABR48242). Bladder cancer-associated sequences from the present invention
CC have cytostatic activities, and can be used in antisense gene therapy and
CC in vaccine production. The method can be used for detecting a bladder
CC cancer-associated transcript in a cell from a patient. The method is
CC useful in diagnosing or treating bladder cancer and in screening for
CC compounds that modulate bladder cancer, such as hormones or antibodies.
CC The nucleic acid molecules from the present invention may be used in
CC various screening and diagnostic methods, and for gene therapy, vaccine
CC and/or antisense/inhibition applications
XX
SQ Sequence 359 AA;

Query Match 100.0%; Score 275; DB 6; Length 359;
Best Local Similarity 100.0%; Pred. No. 8e-26;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLYSYTTDGNVTSSDGLWNNNTQLFLEHSLLTANTTKGIYAGVCISVL 52
|||||
Db 249 PLYSYTTDGNVTSSDGLWNNNTQLFLEHSLLTANTTKGIYAGVCISVL 300

RESULT 10
AAO26680
ID AAO26680 standard; protein; 359 AA.
XX
XX AAO26680;
AC
XX
XX 20-MAR-2003 (first entry)
DT
XX
XX KIM-1 related protein, SEQ ID No 8.
DE

XX Cytostatic; gene therapy; antibody; antigen; antigen-binding;
KW proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;
KW renal disease; injury; renal cancer; human.
XX Homo sapiens.
XX WO200298920-A1.
XX
PD 12-DEC-2002.
XX
XX 31-MAY-2002; 2002WO-US017402.
XX
XX 01-JUN-2001; 2001US-0295449P.
XX 04-JUN-2001; 2001US-0295907P.
XX
XX (BIO) BIOGEN INC.
XX (GEO) GEN HOSPITAL CORP.
XX
XX Bailly V, Bonventre J;
XX WPI; 2003-156845/15.
XX
XX New antibody, antibody derivative or antigen-binding polypeptide that
PT inhibits proteolytic release of a soluble kidney injury molecule-1
PT polypeptide, useful for treating or preventing renal disease or injury,
PT e.g. renal cancer.
XX
XX Disclosure; Page 40-41; 42pp; English.
XX
XX The invention relates to a novel antibody, antibody derivative or antigen
CC binding polypeptide that inhibits proteolytic release of a soluble
CC kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.
CC The antibody, antibody derivative or antigen-binding polypeptide is
CC useful for treating or preventing renal disease or injury, e.g. renal
CC cancer. The antibody is also useful for inhibiting shedding of the KIM-1
CC polypeptide. This sequence represents a protein relating to the KIM-1
CC protein of the invention
XX
XX Sequence 359 AA;
SQ
Query Match 100.0%; Score 275; DB 6; Length 359;
Best Local Similarity 100.0%; Pred. No. 8e-26;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PLYSYTGDNDVTVESSDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 52
Db 249 PLYSYTGDNDVTVESSDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 300
RESULT 11
ADE36594
ID ADE36594 standard; protein; 359 AA.
XX
XX ADE36594;
XX
XX 29-JAN-2004 (first entry)
XX
XX Human NOV1b protein SEQ ID NO:4.
XX
XX human; NOVX; cytostatic; antiinflammatory; gene therapy; vaccine;
KW renal cancer; inflammation; tissue typing.
XX
XX Homo sapiens.
XX
XX WO2003080856-A2.
XX
XX 02-OCT-2003.
XX
XX 19-MAR-2003; 2003WO-US008490.
XX
XX 19-MAR-2002; 2002US-0365491P.
XX 13-SEP-2002; 2002US-0410618P.

XX (CURA-) CURAGEN CORP.
XX
XX Lepley DM, Rieger DK, Tse K, Rastelli L, Smithson G, Mesri M;
PI Ooi CE, Anderson DW, Guo X, Giot L, Starling G;
XX
XX WPI; 2003-876927/81.
XX N-PSDB; ADE36593.
XX
XX New polypeptide, useful for preparing a composition for treating or
PT preventing a pathology associated with NOVX polypeptide e.g. renal cancer
PT or inflammation, or for tissue typing.
XX
XX Claim 1; SEQ ID NO 4; 239pp; English.
XX
XX The present invention describes an isolated human NOVX polypeptide, where
CC x is la to 1d or 2a to 2h, or its mature form, a sequence that is at
CC least 95 % identical to it, or a sequence comprising one or more
CC conservative substitutions in the amino acid sequence. The NOVX
CC polypeptide, and nucleic acid sequence encoding it, has cytostatic and
CC antiinflammatory activities, and can be used in gene therapy, and in
CC vaccines. The NOVX polypeptide is useful for preparing a composition for
CC treating or preventing a pathology associated with NOVX polypeptide e.g.
CC renal cancer or inflammation, or for tissue typing. The present sequence
CC represents human NOV1b from the present invention.
XX
XX Sequence 359 AA;
SQ
Query Match 100.0%; Score 275; DB 7; Length 359;
Best Local Similarity 100.0%; Pred. No. 8e-26;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PLYSYTGDNDVTVESSDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 52
Db 249 PLYSYTGDNDVTVESSDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 300
RESULT 12
ADN38984
ID ADN38984 standard; protein; 359 AA.
XX
XX ADN38984;
XX
XX 17-JUN-2004 (first entry)
XX
XX Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:302.
XX
XX Human; differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW retinal neovascularisation syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW vulnery; gene therapy; vaccine.
XX
XX Homo sapiens.
XX
XX WO2003042661-A2.
XX
XX 22-MAY-2003.
XX
XX 13-NOV-2002; 2002WO-US036810.
XX
XX 13-NOV-2001; 2001US-0350666P.
XX 21-NOV-2001; 2001US-0332464P.
XX 29-NOV-2001; 2001US-0334393P.
XX 03-DEC-2001; 2001US-0335394P.
XX 14-DEC-2001; 2001US-0340376P.
XX 08-JAN-2002; 2002US-0347211P.
XX 10-JAN-2002; 2002US-0347349P.
XX 08-FEB-2002; 2002US-0355250P.
XX 13-FEB-2002; 2002US-0356714P.
XX 20-FEB-2002; 2002US-0359077P.

PR 29-MAR-2002; 2002US-0368809P.
 PR 04-APR-2002; 2002US-0370110P.
 PR 12-APR-2002; 2002US-0372246P.
 PR 05-JUN-2002; 2002US-0386614P.
 PR 16-JUL-2002; 2002US-0396839P.
 PR 22-JUL-2002; 2002US-0397775P.
 PR 22-JUL-2002; 2002US-0397845P.
 PR 09-SEP-2002; 2002US-0409450P.
 XX (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 XX Afar D, Aziz N, Gineburg WM, Gish KC, Glynne R, Hevezil PA;
 PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
 XX N-PSDB; ADN38983.
 DR WPI; 2003-468649/44.
 DR
 DR
 XX Determining the presence or absence of a pathological cell in a patient,
 PT useful for diagnosing, prognosing or treating cancer, comprises detecting
 PT a nucleic acid in a biological sample.
 XX
 XX Claim 12; SEQ ID NO 302; 1385pp; English.
 PS
 XX
 XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
 CC whose expression is upregulated or downregulated in specific cancers or
 CC other diseases such as angiogenic or fibrotic disorders, and to methods
 CC of determining the presence or absence of a pathological cell in a
 CC patient by detecting a nucleic acid at least 80% identical to those of
 CC the invention or by detecting a polypeptide of the invention. The
 CC invention also relates to expression vectors and host cells comprising a
 CC nucleic acid of the invention; antibodies which specifically bind a
 CC polypeptide of the invention; use of such antibodies for drug targeting;
 CC and methods of screening for modulators of activity or expression of the
 CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
 CC antibodies and methods are useful for diagnosing, prognosing and treating
 CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
 CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
 CC neovascularisation syndromes, scarring and uterine fibroids. They may
 CC also be useful in wound healing and in contraception. The present
 CC sequence represents a polypeptide of the invention.
 XX
 XX Sequence 359 AA;
 SQ
 Query Match 100.0%; Score 275; DB 7; Length 359;
 Best Local Similarity 100.0%; Pred. No. 8e-26;
 Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PLYSYTDCNDVTWESSDGLWNNQTLFLEHSLTANTTKGIYAGVCISVL 52
 DB 249 PLYSYTDCNDVTWESSDGLWNNQTLFLEHSLTANTTKGIYAGVCISVL 300
 RESULT 13
 ADQ76690
 ID ADQ76690 standard; protein; 359 AA.
 XX
 AC ADQ76690;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Human kidney injury molecule-1 (KIM-1).
 XX
 KW Human; KIM-1; kidney injury molecule-1; immunosuppressive; protozoacide;
 KW muscular-gen.; neuroprotective; antianaemic; antithyroid; haemostatic;
 KW antiallergic; antiinflammatory; vasotropic; nephrotic.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..20
 FT /label= Signal_peptide
 FT Modified-site 65..67
 FT /note= "N-glycosylated"

FT Modified-site 258..260
 /note= "N-glycosylated"
 FT Modified-site 272..274
 /note= "N-glycosylated"
 FT Modified-site 286..288
 /note= "N-glycosylated"
 FT Domain 290..311
 /note= "Transmembrane domain"
 FT Region 324..359
 /note= "C-terminal region unique to this splice variant"
 XX
 XX WO2004060041-A2.
 XX 22-JUL-2004.
 XX 29-DEC-2003; 2003WO-US041294.
 XX 30-DEC-2002; 2002US-0436934P.
 XX (BIOG-) BIOGEN IDEC MA INC.
 XX Remmert PD;
 XX WPI; 2004-534277/51.
 XX
 XX Use of a kidney injury molecule-1 (KIM-1) antagonist for e.g. treating
 PT Th2 cell-mediated diseases or inflammatory diseases, inhibiting B cell
 PT activation, or inhibiting production of a subset of antibodies against
 PT one or more antigens.
 XX
 PS Disclosure; SEQ ID NO 1; 68pp; English.
 XX
 XX The present sequence is that of human kidney injury molecule-1 (KIM-1), a
 CC type I cell membrane glycoprotein and member of the T cell immunoglobulin
 CC (Ig) and mucin domain (TIM) family. This protein has 334 amino acids
 CC ADQ76696 or 359 amino acids, depending on splice variation. It has been
 CC discovered that treatment of a mammal with a KIM-1 antagonist alters the
 CC interaction of T cells and other immune system cells, e.g. dendritic
 CC cells, monocytes, macrophages and B cells, and thereby strongly
 CC suppresses an IgG response to an antigen. Such treatment also eliminates
 CC IgG1 production by memory B cells in response to subsequent challenge
 CC with the antigen. Blockage of the binding of KIM-1 to its receptor
 CC reduces secretion of interferon-gamma by immune cells engaged in an
 CC antigen response in the mixed lymphocyte response assay. Based on these
 CC discoveries, the invention provides methods for therapeutically
 CC modulating immune function in autoimmune diseases and other disorders of
 CC the mammalian immune system. A method is claimed for inhibiting
 CC signalling between a T cell and a second cell, e.g. an antigen-presenting
 CC cell, in a mammal. The method involves identifying a mammal with an
 CC immune disease or disorder, or one preparing to receive a tissue graft,
 CC and administering a KIM-1 antagonist, especially a polypeptide
 CC comprising: a KIM-1 Ig domain, and lacking a transmembrane domain and a
 CC KIM-1 cytoplasmic domain; an anti-KIM-1 antibody; or an antigen-binding
 CC fragment of an anti-KIM-1 antibody. Preferably, the KIM-1 antagonist is a
 CC soluble polypeptide, which can include a KIM-1 mucin domain in addition
 CC to the KIM Ig domain, and may include a heterologous moiety such as an Fc
 CC moiety. The antagonist may be conjugated to a polymer such as
 CC polyethylene glycol. The KIM-1 antagonist is used in methods of:
 CC inhibiting activation of a B cell in a mammal; inhibiting disease relapse
 CC in an autoimmune disease; inhibiting epicope spreading in an autoimmune
 CC disease; treating a Th2 cell-mediated disease (e.g. myasthenia gravis,
 CC autoimmune haemolytic anaemia, Chagas disease, Grave's disease,
 CC idiopathic thrombocytopenia purpura, Wegener's granulomatosis,
 CC polyarteritis nodosa, rapidly progressive crescentic glomerulonephritis,
 CC graft-versus-host disease, or systemic lupus nephritis) or inflammatory
 CC disease or disorder (e.g. inflammatory bowel diseases such as Crohn's
 CC disease, ulcerative colitis, and ileitis); and inhibiting secretion of
 CC IFN-gamma by lymphocytes.
 XX
 SQ Sequence 359 AA;
 Query Match 100.0%; Score 275; DB 8; Length 359;
 Best Local Similarity 100.0%; Pred. No. 8e-26;

Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLYSYTTDGNVTVESSDGLWNNQTQLFLEHSLLTANTTKGIYAGVCISVL 52
DB 249 PLYSYTTDGNVTVESSDGLWNNQTQLFLEHSLLTANTTKGIYAGVCISVL 300

RESULT 14
ABP70442
ID ABP70442 standard; protein; 364 AA.
AC ABP70442;
XX
DT 22-APR-2003 (first entry)
XX
DE Amino acid sequence of human TIM-1 allele 5.
XX
KW T cell immunoglobulin domain; mucin domain; TIM; TIM-1; TIM-2; TIM-3;
KW TIM-4; immune dysfunction; chromosome 5; malignancy; allergy; eczema;
KW myelodysplastic syndrome; airway hyperreactivity; cancer; asthma;
KW allergic T cell response; autoimmune disease.
XX
OS Homo sapiens.
XX
FN WO2003002722-A2.
XX
PD 09-JAN-2003.
XX
PF 01-JUL-2002; 2002WO-US020890.
XX
PR 29-JUN-2001; 2001US-0302344P.
XX
PA (STRD) UNIV LELAND STANFORD JUNIOR.
XX
PI McIntire JJ, Dekruyff RH, Umetsu DT, Freeman GJ, Kuchroo V;
XX
DR WPI; 2003-210268/20.
DR N-PSDB; ABZ68336.
XX
PT New nucleic acid comprising a mammalian T cell immunoglobulin domain and
PT Mucin domain gene sequences, useful for treating cancer or asthma,
PT allergy, eczema or autoimmune disease.
XX
PS Claim 10; Page 86-87; 94pp; English.
XX
CC The present sequence is a human T cell immunoglobulin domain and mucin
CC domain-1 (TIM-1) polypeptide. The specification describes TIM-1, TIM-2,
CC TIM-3 and TIM-4. TIM polypeptides are cell surface molecules with
CC conserved IGV and mucin domains. The locus comprising the TIM family is
CC genetically associated with immune dysfunction, including asthma. The TIM
CC gene family is located within a region of human chromosome 5 that is
CC commonly deleted in malignancies and myelodysplastic syndrome. Variants
CC of TIM-1 and TIM-3 are associated with susceptibility to airway
CC hyperreactivity and allergic T cell responses, and other variants
CC associated with protection against these responses. T cells express TIM
CC proteins, which critically regulate CD4 T cell differentiation. Th1 cells
CC preferentially express TIM-3, while Th2 cells preferentially express TIM-
CC 1. TIM polypeptides and polynucleotides are useful for treating cancer,
CC asthma, allergies, eczema or autoimmune diseases
XX
SQ Sequence 364 AA;

Query Match 100.0%; Score 275; DB 6; Length 364;
Best Local Similarity 100.0%; Pred. No. 8.1e-26;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLYSYTTDGNVTVESSDGLWNNQTQLFLEHSLLTANTTKGIYAGVCISVL 52
DB 254 PLYSYTTDGNVTVESSDGLWNNQTQLFLEHSLLTANTTKGIYAGVCISVL 305

RESULT 15
ABP70440

ID ABP70440 standard; protein; 365 AA.
XX
AC ABP70440;
XX
DT 22-APR-2003 (first entry)
XX
DE Amino acid sequence of human TIM-1 allele 3.
XX
KW T cell immunoglobulin domain; mucin domain; TIM; TIM-1; TIM-2; TIM-3;
KW TIM-4; immune dysfunction; chromosome 5; malignancy; allergy; eczema;
KW myelodysplastic syndrome; airway hyperreactivity; cancer; asthma;
KW allergic T cell response; autoimmune disease.
XX
OS Homo sapiens.
XX
FN Key Location/Qualifiers
FT Misc-difference 208 /note= "encoded by RCG"
XX
PN WO2003002722-A2.
XX
PD 09-JAN-2003.
XX
PF 01-JUL-2002; 2002WO-US020890.
XX
PR 29-JUN-2001; 2001US-0302344P.
XX
PA (STRD) UNIV LELAND STANFORD JUNIOR.
XX
PI McIntire JJ, Dekruyff RH, Umetsu DT, Freeman GJ, Kuchroo V;
XX
DR WPI; 2003-210268/20.
DR N-PSDB; ABZ68334.
XX
PT New nucleic acid comprising a mammalian T cell immunoglobulin domain and
PT Mucin domain gene sequences, useful for treating cancer or asthma,
PT allergy, eczema or autoimmune disease.
XX
PS Claim 10; Page 83-84; 94pp; English.
XX
CC The present sequence is a human T cell immunoglobulin domain and mucin
CC domain-1 (TIM-1) polypeptide. The specification describes TIM-1, TIM-2,
CC TIM-3 and TIM-4. TIM polypeptides are cell surface molecules with
CC conserved IGV and mucin domains. The locus comprising the TIM family is
CC genetically associated with immune dysfunction, including asthma. The TIM
CC gene family is located within a region of human chromosome 5 that is
CC commonly deleted in malignancies and myelodysplastic syndrome. Variants
CC of TIM-1 and TIM-3 are associated with susceptibility to airway
CC hyperreactivity and allergic T cell responses, and other variants
CC associated with protection against these responses. T cells express TIM
CC proteins, which critically regulate CD4 T cell differentiation. Th1 cells
CC preferentially express TIM-3, while Th2 cells preferentially express TIM-
CC 1. TIM polypeptides and polynucleotides are useful for treating cancer,
CC asthma, allergies, eczema or autoimmune diseases
XX
SQ Sequence 365 AA;

Query Match 100.0%; Score 275; DB 6; Length 365;
Best Local Similarity 100.0%; Pred. No. 8.2e-26;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLYSYTTDGNVTVESSDGLWNNQTQLFLEHSLLTANTTKGIYAGVCISVL 52
DB 255 PLYSYTTDGNVTVESSDGLWNNQTQLFLEHSLLTANTTKGIYAGVCISVL 306

Search completed: June 29, 2005, 09:09:09
Job time : 37.9823 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 08:57:16 ; Search time 7.15128 Seconds
(without alignments)
542.805 Million cell updates/sec

Title: US-10-718-321-7_COPY_249_300

Perfect score: 275

Sequence: 1 PLYSVTTGNDVTETSSDGL.....SLLTANTTKGIYAGVCISVL 52

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/1aa/5A-COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep.*
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- 4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS-COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	275	100.0	334	4	US-09-197-970B-7
2	228	82.9	451	1	US-08-287-001A-2
3	228	82.9	451	5	PCT-US95-09941-2
4	78	28.4	307	4	US-09-197-970B-3
5	62	22.5	606	4	US-09-603-208A-56
6	60	21.8	602	1	US-08-168-091A-2
7	60	21.8	602	1	US-08-428-926-5
8	60	21.8	602	1	US-08-428-927-5
9	60	21.8	602	1	US-08-428-298-5
10	60	21.8	602	1	US-08-339-517-5
11	60	21.8	1070	3	US-08-697-954-2
12	60	21.8	1260	4	US-09-328-352-6746
13	58	21.1	981	4	US-09-991-258-13
14	56.5	20.5	1039	4	US-09-270-767-41514
15	55.5	20.2	137	4	US-09-540-236-2771
16	55.5	20.2	495	4	US-09-691-270A-24
17	55	20.0	386	4	US-09-328-352-8185
18	55	20.0	463	4	US-09-375-140-10
19	55	20.0	548	4	US-09-375-140-11
20	54.5	19.8	323	6	5260223-4
21	54.5	19.8	323	6	5260223-4
22	54.5	19.8	1619	4	US-09-328-352-7347
23	54	19.6	357	4	US-09-248-796A-21669
24	53.5	19.5	72	4	US-09-489-847-366
25	53.5	19.5	73	4	US-09-489-847-241
26	53.5	19.5	224	4	US-09-248-796A-18758
27	53.5	19.5	10182	3	US-09-134-001C-3159

28	53	19.3	112	3	US-09-134-001C-3352	Sequence 3352, Ap
29	53	19.3	190	3	US-08-341-018-44	Sequence 44, Appl
30	53	19.3	190	3	US-08-470-335-217	Sequence 217, App
31	53	19.3	190	3	US-08-470-339-217	Sequence 217, App
32	53	19.3	190	4	US-08-467-602-411	Sequence 411, App
33	53	19.3	210	4	US-08-467-602-191	Sequence 191, App
34	53	19.3	210	4	US-08-411-295F-315	Sequence 315, App
35	53	19.3	213	4	US-08-467-603-186	Sequence 186, App
36	53	19.3	213	4	US-08-411-295F-310	Sequence 310, App
37	53	19.3	219	4	US-08-467-602-200	Sequence 200, App
38	53	19.3	219	4	US-08-411-295F-324	Sequence 324, App
39	53	19.3	222	4	US-08-467-602-197	Sequence 197, App
40	53	19.3	222	4	US-08-411-295F-321	Sequence 321, App
41	53	19.3	233	4	US-08-467-603-194	Sequence 194, App
42	53	19.3	233	4	US-08-411-295F-318	Sequence 318, App
43	53	19.3	242	4	US-08-467-602-203	Sequence 203, App
44	53	19.3	242	4	US-08-411-295F-327	Sequence 327, App
45	53	19.3	309	4	US-09-248-796A-25339	Sequence 25339, A

ALIGNMENTS

RESULT 1

US-09-197-970B-7

; Sequence 7, Application US/09197970B

; Patent No. 6664385

; GENERAL INFORMATION:

; APPLICANT: Michele Sanicola-Nadel

; Joseph V. Bonventre

; Catherine A. Hession

; Takaharu Ichimura

; Henry Wei

; Richard L. Cate

; TITLE OF INVENTION: MODULATORS OF TISSUE REGENERATION

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Biogen, Inc.

; STREET: 14 Cambridge Center

; CITY: Cambridge

; STATE: MA

; COUNTRY: USA

; ZIP: 02142

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09197,970B

; FILING DATE: 23-No. 6664385-1998

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/018,228

; FILING DATE: 24-MAY-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Levine, Leslie M.

; REGISTRATION NUMBER: 35,245

; REFERENCE/DOCKET NUMBER: A010 PCT CIP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 679-2810

; TELEFAX: (617) 679-2838

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 334 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-197-970B-7
Query Match 100.0%; Score 275; DB 4; Length 334;
Best Local Similarity 100.0%; Pred. No. 1.2e-28;

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Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLYSVTTDGNVTVESSDGLWNNNTQLFLEHSLTANTTKGIYAGVCISVL 52
    |||||||
Db 249 PLYSVTTDGNVTVESSDGLWNNNTQLFLEHSLTANTTKGIYAGVCISVL 300
    |||||||

RESULT 2
US-08-287-001A-2
; Sequence 2, Application US/08287001A
; Patent No. 5622861
; GENERAL INFORMATION:
; APPLICANT: KAPLAN, GERARDO
; APPLICANT: PEINSTONE, STEPHEN M.
; TITLE OF INVENTION: HEPATITIS A VIRUS RECEPTOR AND METHODS
; TITLE OF INVENTION: OF USE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, The Candler Bldg, 127 Peachtree
; STREET: Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/287,001A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Spratt, Gwedolyn D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 1414.621
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US-287-001A-2

Query Match 82.9%; Score 228; DB 1; Length 451;
Best Local Similarity 84.6%; Pred. No. 3.5e-22;
Matches 44; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 PLYSVTTDGNVTVESSDGLWNNNTQLFLEHSLTANTTKGIYAGVCISVL 52
    |||||||
Db 329 PLYSVTTDGNVTVESSDGLWNNNTQLFLEHSLTANTTKGIYAGVCISVL 380
    |||||||

RESULT 3
PCT-US95-09941-2
; Sequence 2, Application PC/TUS9509941
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HEPATITIS A VIRUS RECEPTOR AND METHODS
; TITLE OF INVENTION: OF USE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, The Candler Bldg, 127 Peachtree
; STREET: Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA

Query Match 82.9%; Score 228; DB 1; Length 451;
Best Local Similarity 84.6%; Pred. No. 3.5e-22;
Matches 44; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 PLYSVTTDGNVTVESSDGLWNNNTQLFLEHSLTANTTKGIYAGVCISVL 52
    |||||||
Db 329 PLYSVTTDGNVTVESSDGLWNNNTQLFLEHSLTANTTKGIYAGVCISVL 380
    |||||||

RESULT 4
US-09-197-970B-3
; Sequence 3, Application US/09197970B
; Patent No. 6664385
; GENERAL INFORMATION:
; APPLICANT: Michele Sanicola-Nadel
; Joseph V. Bonventre
; Catherine A. Hession
; Takaharu Ichimura
; Henry Wei
; Richard L. Cate
; TITLE OF INVENTION: MODULATORS OF TISSUE REGENERATION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/197,970B
; FILING DATE: 23-NO. 6664385-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/018,228
; FILING DATE: 24-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Levine, Leslie M.
; REGISTRATION NUMBER: 35,245
; REFERENCE/DOCKET NUMBER: A010 PCT CIP
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; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09941
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/287,001
; FILING DATE: 5 AUG 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Spratt, Gwedolyn D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 1414.621
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-09941-2

Query Match 82.9%; Score 228; DB 5; Length 451;
Best Local Similarity 84.6%; Pred. No. 3.5e-22;
Matches 44; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 PLYSVTTDGNVTVESSDGLWNNNTQLFLEHSLTANTTKGIYAGVCISVL 52
    |||||||
Db 329 PLYSVTTDGNVTVESSDGLWNNNTQLFLEHSLTANTTKGIYAGVCISVL 380
    |||||||

RESULT 4
US-09-197-970B-3
; Sequence 3, Application US/09197970B
; Patent No. 6664385
; GENERAL INFORMATION:
; APPLICANT: Michele Sanicola-Nadel
; Joseph V. Bonventre
; Catherine A. Hession
; Takaharu Ichimura
; Henry Wei
; Richard L. Cate
; TITLE OF INVENTION: MODULATORS OF TISSUE REGENERATION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/197,970B
; FILING DATE: 23-NO. 6664385-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/018,228
; FILING DATE: 24-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Levine, Leslie M.
; REGISTRATION NUMBER: 35,245
; REFERENCE/DOCKET NUMBER: A010 PCT CIP
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 679-2810
TELEFAX: (617) 679-2838
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-197-9708-3

Query Match 28.4%; Score 78; DB 4; Length 307;
Best Local Similarity 42.0%; Pred. No. 0.026;
Matches 21; Conservative 7; Mismatches 18; Indels 4; Gaps 3;

QY 4 SYT-DGNDVTSSDGLWNNNOTQLFLEHSLLTANTTKGIYAGVCISVL 52
DB 199 SYTPADWNGTVT-SSEAWNNHTVRIPLRKP--QRNPTKGFVGMVAAL 245

RESULT 5

US-09-603-208A-56
Sequence 56, Application US/09603208A
Patent No. 6822084

GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
APPLICANT: Lee, Heung-Shick
APPLICANT: Kim, Hyung-Joon
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS,
TITLE OF INVENTION: RESISTANCE AND TOLERANCE PROTEINS
FILE REFERENCE: BGI-124CP

CURRENT APPLICATION NUMBER: US/09/603,208A
CURRENT FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/142692
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: 60/151214
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19930429.7
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: DE 19931413.6
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931457.8
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931541.8
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19932209.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932230.9
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932914.1
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19940764.9
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19941382.7
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 306
SEQ ID NO 56
LENGTH: 606
TYPE: PRT
ORGANISM: Corynebacterium glutamicum

US-09-603-208A-56

Query Match 22.5%; Score 62; DB 4; Length 606;
Best Local Similarity 32.6%; Pred. No. 8.7;
Matches 14; Conservative 5; Mismatches 24; Indels 0; Gaps 0;

QY 1 PLYSYTTDGNDFVTSSDGLWNNNOTQLFLEHSLLTANTTKGI 43
DB 559 PLVEYQKGGDMFNGMKDGIKEETVRQLFSLSSSSSKTRKSL 601

RESULT 6

US-08-168-091A-2
Sequence 2, Application US/08168091A
Patent No. 5665862

GENERAL INFORMATION:
APPLICANT: Fischbach, Gerald.
APPLICANT: Falls, Douglas R.
APPLICANT: Rosen, Kenneth M.
APPLICANT: Corfaa, Gabriel
TITLE OF INVENTION: Neurotrophic Factor
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE AND COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,091A
FILING DATE: 15-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/953,742
FILING DATE: 29-SEP-1992

ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: HMI-002CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 602 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-168-091A-2

Query Match 21.8%; Score 60; DB 1; Length 602;
Best Local Similarity 31.7%; Pred. No. 16;
Matches 13; Conservative 11; Mismatches 15; Indels 2; Gaps 1;

QY 3 YSYTTDGNDFVTSSDGLWNNNOTQLFLEHSLLTANTTK 41
DB 301 YTSITTHSMVTVTQTPSHKSNIGHTSILSESHSVLVSSSVE 341

RESULT 7

US-08-428-926-5
Sequence 5, Application US/08428926
Patent No. 5667780

GENERAL INFORMATION:
APPLICANT: Ho, Wei-Hsien
APPLICANT: Osheroif, Phyllis L.
TITLE OF INVENTION: SENSORY AND MOTOR NEURON DERIVED FACTOR (SMDF)
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California

```

; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-428-927-5

Query Match                21.8%; Score 60; DB 1; Length 602;
Best Local Similarity      31.7%; Pred. No. 16;
Matches 13; Conservative 11; Mismatches 15; Indels 2; Gaps 1;

QY    3 YSYTTDGNNTVTVSSDGLMNNNOTQLFL--EHSLLTANTTK 41
      |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~::~::
DB    301 YTSTTHSMVTQTTPSHSWSNGHTESILSESHSVLVSSSVE 341

RESULT 9
US-08-428-298-5
; Sequence 5, Application US/08428298
; Patent No. 5763213
; GENERAL INFORMATION:
; APPLICANT: Ho, Wei-Hsien
; APPLICANT: Osherooff, Phyllis L.
; TITLE OF INVENTION: SENSORY AND MOTOR NEURON DERIVED FACTOR (SMDF)
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,298
; FILING DATE: 25-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/339517
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 853D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-428-298-5

Query Match                21.8%; Score 60; DB 1; Length 602;
Best Local Similarity      31.7%; Pred. No. 16;
Matches 13; Conservative 11; Mismatches 15; Indels 2; Gaps 1;

QY    3 YSYTTDGNNTVTVSSDGLMNNNOTQLFL--EHSLLTANTTK 41
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DB    301 YTSTTHSMVTQTTPSHSWSNGHTESILSESHSVLVSSSVE 341

RESULT 10
US-08-339-517-5
; Sequence 5, Application US/08339517
; Patent No. 5770567
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[illegible]

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; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 981
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; No. 6783939e =
; OTHER INFORMATION: synthetic construct
US-09-991-258-13

Query Match      21.1%; Score 58; DB 4; Length 981;
Best Local Similarity 47.6%; Pred. No. 55;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 11 DTVTSSDGLWNNNQTLFLE 31
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Db 484 ETTWESLDHLWNNNQMFVIQ 504

RESULT 14
US-09-270-767-41514
; Sequence 41514, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41514
; LENGTH: 1039
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-41514

Query Match      20.5%; Score 56.5; DB 4; Length 1039;
Best Local Similarity 31.8%; Pred. No. 94;
Matches 14; Conservative 10; Mismatches 17; Indels 3; Gaps 1;

QY 6 TTGNDVTSSDGLWNNNQTLFLEHSLLTANTTKGIYAGVCI 49
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Db 219 TSAGNSTSADNSTPKDNSTAQLLAD---LATINFEETIFABICL 259

RESULT 15
US-09-540-236-2771
; Sequence 2771, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARACTAE
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2771
; LENGTH: 137
; TYPE: PRT
; ORGANISM: M.cattarrhalis
US-09-540-236-2771

Query Match      20.2%; Score 55.5; DB 4; Length 137;
Best Local Similarity 31.7%; Pred. No. 9.8;
Matches 13; Conservative 8; Mismatches 15; Indels 5; Gaps 1;

QY 9 GNDVTSSDGLWNNNQTLF-----LEHSLLTANTTKGIY 44
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Db 86 GTVAIKQKADSLANHLQTRRFRGLELLAHSIINVPSNDGIY 126

Search completed: June 29, 2005, 09:02:59
Job time : 7.15128 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 29, 2005, 08:58:20 ; Search time 32.5894 Seconds
(without alignments)
613.589 Million cell updates/sec

Title: US-10-718-321-7_COPY_249_300

Perfect score: 275

Sequence: 1 PLYSYTDCGNTVTSSDGL.....SLLTANTTKGIYAGVCISVL 52

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Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	275	100.0	334	17	US-10-655-506-7
2	275	100.0	334	17	US-10-718-321-7
3	275	100.0	339	17	US-10-391-939A-2
4	275	100.0	339	17	US-10-391-939A-28
5	275	100.0	359	14	US-10-188-012-17
6	275	100.0	359	14	US-10-188-012-19
7	275	100.0	359	15	US-10-295-027-302
8	275	100.0	359	15	US-10-188-832-64
9	275	100.0	359	17	US-10-391-939A-4
10	275	100.0	359	17	US-10-663-497-17
11	275	100.0	359	17	US-10-663-497-19

12	275	100.0	359	17	US-10-718-321-8	Sequence 8, Appli
13	275	100.0	359	17	US-10-847-918-25	Sequence 25, Appl
14	275	100.0	364	14	US-10-188-012-25	Sequence 25, Appl
15	275	100.0	364	17	US-10-663-497-25	Sequence 25, Appl
16	275	100.0	365	14	US-10-188-012-21	Sequence 21, Appl
17	275	100.0	365	17	US-10-663-497-21	Sequence 21, Appl
18	270	98.2	359	14	US-10-188-012-23	Sequence 23, Appl
19	270	98.2	359	17	US-10-663-497-23	Sequence 23, Appl
20	270	98.2	364	14	US-10-188-012-27	Sequence 27, Appl
21	270	98.2	364	17	US-10-663-497-27	Sequence 27, Appl
22	225	81.8	81	17	US-10-718-321-6	Sequence 6, Appli
23	189	68.7	263	17	US-10-391-939A-6	Sequence 6, Appli
24	189	68.7	263	17	US-10-391-939A-32	Sequence 32, Appl
25	189	68.7	263	17	US-10-391-939A-39	Sequence 39, Appl
26	189	68.7	263	17	US-10-805-177-50	Sequence 50, Appl
27	99	36.0	18	17	US-10-718-321-1	Sequence 1, Appli
28	79	28.7	305	14	US-10-188-012-1	Sequence 1, Appli
29	79	28.7	305	17	US-10-663-497-1	Sequence 1, Appli
30	78	28.4	307	17	US-10-655-506-3	Sequence 3, Appli
31	76.5	27.8	282	14	US-10-188-012-3	Sequence 3, Appli
32	76.5	27.8	282	17	US-10-663-497-3	Sequence 3, Appli
33	66	24.0	666	16	US-10-437-963-196644	Sequence 196644,
34	65	23.6	554	14	US-10-125-692-21	Sequence 21, Appl
35	60.5	22.0	727	16	US-10-296-723A-14	Sequence 14, Appl
36	60	21.8	244	15	US-10-424-599-239255	Sequence 239255,
37	60	21.8	285	15	US-10-424-599-255038	Sequence 255038,
38	60	21.8	338	15	US-10-425-114-37036	Sequence 37036, A
39	60	21.8	338	15	US-10-412-699B-514	Sequence 514, App
40	59.5	21.6	125	15	US-10-424-599-220078	Sequence 220078,
41	58.5	21.6	305	14	US-10-188-012-5	Sequence 5, Appli
42	59.5	21.6	305	14	US-10-188-012-7	Sequence 7, Appli
43	59.5	21.6	305	17	US-10-663-497-5	Sequence 5, Appli
44	59.5	21.6	305	17	US-10-663-497-7	Sequence 7, Appli
45	58	21.1	272	16	US-10-425-115-288232	Sequence 288232,

ALIGNMENTS

RESULT 1

US-10-655-506-7
; Sequence 7, Application US/10655506
; Publication No. US20050089868A1
; GENERAL INFORMATION:
; APPLICANT: Michele Sanicola-Nadel
; Joseph V. Bonventre
; Catherine A. Heslon
; Takaharu Ichimura
; Henry Wei
; Richard L. Cate
; TITLE OF INVENTION: MODULATORS OF TISSUE REGENERATION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/655,506
; FILING DATE: 04-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/197,970
; FILING DATE: 23-Nov-1998
; APPLICATION NUMBER: US 60/018,228
; FILING DATE: 24-MAY-1996

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Levine, Leslie M.
; REGISTRATION NUMBER: 35,245
; REFERENCE/DOCKET NUMBER: A010 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 679-2810
; TELEFAX: (617) 679-2838
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 334 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-655-506-7

Query Match          100.0%; Score 275; DB 17; Length 334;
Best Local Similarity 100.0%; Pred. No. 4.2e-28;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLYSYTTDGDNDVTVESSDGLWNNNTQLFLEHSLLTANTTTKGIYAGVCISVL 52
DB 249 PLYSYTTDGDNDVTVESSDGLWNNNTQLFLEHSLLTANTTTKGIYAGVCISVL 300

RESULT 2
US-10-718-321-7
; Sequence 7, Application US/10718321
; Publication No. US20050112117A1
; GENERAL INFORMATION:
; APPLICANT: Biogen Idec Ma Inc.
; APPLICANT: Bailly, Veronique
; APPLICANT: Bonventre, Joseph
; TITLE OF INVENTION: The General Hospital Corporation
; TITLE OF INVENTION: Molecules and Methods for Inhibiting
; FILE REFERENCE: A124 US
; CURRENT APPLICATION NUMBER: US/10/718,321
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/295449
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/295907
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US02/17402
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-718-321-7

Query Match          100.0%; Score 275; DB 17; Length 334;
Best Local Similarity 100.0%; Pred. No. 4.2e-28;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLYSYTTDGDNDVTVESSDGLWNNNTQLFLEHSLLTANTTTKGIYAGVCISVL 52
DB 249 PLYSYTTDGDNDVTVESSDGLWNNNTQLFLEHSLLTANTTTKGIYAGVCISVL 300

RESULT 3
US-10-391-939A-2
; Sequence 2, Application US/10391939A
; Publication No. US20050014687A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W.;
; APPLICANT: Giot, Loic;
; APPLICANT: Guo, Xiaojia Sasha;
; APPLICANT: Lepley, Denise M.;
; APPLICANT: Mesri, Mehdi;
; APPLICANT: Ooi, Chean Eng;
; RESULT 5
US-10-188-012-17
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; Sequence 17, Application US/10188012
; Publication No. US20030124114A1
; GENERAL INFORMATION:
; APPLICANT: McIntire, Jennifer Jones
; APPLICANT: Umetsu, Dale T.
; APPLICANT: Dekruyff, Rosemarie
; APPLICANT: Kuchroo, Vijay
; APPLICANT: Freeman, Gordon J.
; TITLE OF INVENTION: T Cell Regulatory Genes and Methods of
; FILE REFERENCE: STAN-235
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/302,344
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 359
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(360)
; OTHER INFORMATION: TIM-1 allele 1
US-10-188-012-17

Query Match 100.0%; Score 275; DB 14; Length 359;
Best Local Similarity 100.0%; Pred. No. 4.6e-28;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSYTTDGDNDVTSSDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 52
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Db 249 PLSYTTDGDNDVTSSDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 300

RESULT 6

US-10-188-012-19
; Sequence 19, Application US/10188012
; Publication No. US20030124114A1
; GENERAL INFORMATION:
; APPLICANT: McIntire, Jennifer Jones
; APPLICANT: Umetsu, Dale T.
; APPLICANT: Dekruyff, Rosemarie
; APPLICANT: Kuchroo, Vijay
; APPLICANT: Freeman, Gordon J.
; TITLE OF INVENTION: T Cell Regulatory Genes and Methods of
; FILE REFERENCE: STAN-235
; CURRENT APPLICATION NUMBER: US/10/188,012
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/302,344
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 359
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(359)
; OTHER INFORMATION: TIM-1, allele 2
US-10-188-012-19

Query Match 100.0%; Score 275; DB 14; Length 359;
Best Local Similarity 100.0%; Pred. No. 4.6e-28;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSYTTDGDNDVTSSDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 52
|||||
Db 249 PLSYTTDGDNDVTSSDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 300

RESULT 7

US-10-295-027-302
; Sequence 302, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Nataasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 302
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-302

Query Match 100.0%; Score 275; DB 15; Length 359;
Best Local Similarity 100.0%; Pred. No. 4.6e-28;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSYTTDGDNDVTSSDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 52
|||||
Db 249 PLSYTTDGDNDVTSSDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 300

RESULT 8

US-10-188-832-64
; Sequence 64, Application US/10188832
; Publication No. US20040076955A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Nataasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002330US
; CURRENT APPLICATION NUMBER: US/10/188,832
; CURRENT FILING DATE: 2002-11-22

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; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-832-64

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Best Local Similarity 100.0%; Pred. No. 4.6e-28;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSYTTDGDNDVTVESSDGLNANNQTLFLEHSLLTANTTKGIYAGVCISVL 52
Db 249 PLSYTTDGDNDVTVESSDGLNANNQTLFLEHSLLTANTTKGIYAGVCISVL 300

RESULT 9
US-10-391-939A-4
; Sequence 4, Application US/10391939A
; Publication No. US20050014687A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W.;
; APPLICANT: Giot, Loic ;
; APPLICANT: Guo, Xiaojia Sasha;
; APPLICANT: Lepley, Denise M.;
; APPLICANT: Meiri, Mehdi ;
; APPLICANT: Ooi, Chean Eng;
; APPLICANT: Rastelli, Luca ;
; APPLICANT: Rieger, Daniel K.;
; APPLICANT: Smithson, Glenda ;
; APPLICANT: Starling, Gary ;
; APPLICANT: Tse, Kam-Fai
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-048
; CURRENT APPLICATION NUMBER: US/10/391,939A
; CURRENT FILING DATE: 2003-03-19
; PRIOR APPLICATION NUMBER: 60/365,491
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/410,618
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: CuraSeqIst version 0.1
; SEQ ID NO 4
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-391-939A-4

Query Match      100.0%; Score 275; DB 17; Length 359;
Best Local Similarity 100.0%; Pred. No. 4.6e-28;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSYTTDGDNDVTVESSDGLNANNQTLFLEHSLLTANTTKGIYAGVCISVL 52
Db 249 PLSYTTDGDNDVTVESSDGLNANNQTLFLEHSLLTANTTKGIYAGVCISVL 300

RESULT 10
US-10-663-497-17
; Sequence 17, Application US/10663497
; Publication No. US20050095593A1
; GENERAL INFORMATION:
; APPLICANT: Dale Umetsu
; APPLICANT: Rosemarie DeKruyff
; APPLICANT: Jennifer McIntire
; TITLE OF INVENTION: T CELL REGULATORY GENES ASSOCIATED WITH
; FILE REFERENCE: STAN-235CIP
; CURRENT APPLICATION NUMBER: US/10/663,497
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/302,344
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 10/188,012
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 359
; TYPE: PRT
; ORGANISM: H. sapiens
; NAME/KEY: VARIANT
; LOCATION: (1)...(359)
; OTHER INFORMATION: TIM-1, allele 2
US-10-663-497-19

Query Match      100.0%; Score 275; DB 17; Length 359;
Best Local Similarity 100.0%; Pred. No. 4.6e-28;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSYTTDGDNDVTVESSDGLNANNQTLFLEHSLLTANTTKGIYAGVCISVL 52
Db 249 PLSYTTDGDNDVTVESSDGLNANNQTLFLEHSLLTANTTKGIYAGVCISVL 300
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; APPLICANT: Dale Umetsu
; APPLICANT: Rosemarie DeKruyff
; APPLICANT: Jennifer McIntire
; APPLICANT: Gordon Freeman
; TITLE OF INVENTION: T CELL REGULATORY GENES ASSOCIATED WITH
; FILE REFERENCE: STAN-235CIP
; CURRENT APPLICATION NUMBER: US/10/663,497
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/302,344
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 10/188,012
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 359
; TYPE: PRT
; ORGANISM: H. sapiens
; NAME/KEY: VARIANT
; LOCATION: (1)...(360)
; OTHER INFORMATION: TIM-1 allele 1
US-10-663-497-17

Query Match      100.0%; Score 275; DB 17; Length 359;
Best Local Similarity 100.0%; Pred. No. 4.6e-28;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSYTTDGDNDVTVESSDGLNANNQTLFLEHSLLTANTTKGIYAGVCISVL 52
Db 249 PLSYTTDGDNDVTVESSDGLNANNQTLFLEHSLLTANTTKGIYAGVCISVL 300

RESULT 11
US-10-663-497-19
; Sequence 19, Application US/10663497
; Publication No. US20050095593A1
; GENERAL INFORMATION:
; APPLICANT: Dale Umetsu
; APPLICANT: Rosemarie DeKruyff
; APPLICANT: Jennifer McIntire
; APPLICANT: Gordon Freeman
; TITLE OF INVENTION: T CELL REGULATORY GENES ASSOCIATED WITH
; FILE REFERENCE: STAN-235CIP
; CURRENT APPLICATION NUMBER: US/10/663,497
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/302,344
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 10/188,012
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 359
; TYPE: PRT
; ORGANISM: H. sapiens
; NAME/KEY: VARIANT
; LOCATION: (1)...(359)
; OTHER INFORMATION: TIM-1, allele 2
US-10-663-497-19

Query Match      100.0%; Score 275; DB 17; Length 359;
Best Local Similarity 100.0%; Pred. No. 4.6e-28;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSYTTDGDNDVTVESSDGLNANNQTLFLEHSLLTANTTKGIYAGVCISVL 52
Db 249 PLSYTTDGDNDVTVESSDGLNANNQTLFLEHSLLTANTTKGIYAGVCISVL 300
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RESULT 12
US-10-718-321-8
; Sequence 8, Application US/10718321
; Publication No. US20050112117A1
; GENERAL INFORMATION:
; APPLICANT: Biogen Idec Ma Inc.
; APPLICANT: Bailly, Veronique
; APPLICANT: Bonventre, Joseph
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: Molecules and Methods for Inhibiting
; TITLE OF INVENTION: Shedding of KIM-1
; FILE REFERENCE: A124 US
; CURRENT APPLICATION NUMBER: US/10/718,321
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/295449
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/295907
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US02/17402
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-718-321-8

Query Match      100.0%; Score 275; DB 17; Length 359;
Best Local Similarity 100.0%; Pred. No. 4.6e-28;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 249 PLYSYTTDGNVTVTSSDGLWNNNTQFLFLEHSLLTANTTKGIYAGVCISVL 300

RESULT 13
US-10-847-918-25
; Sequence 25, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-847-918-25

Query Match      100.0%; Score 275; DB 17; Length 359;
Best Local Similarity 100.0%; Pred. No. 4.6e-28;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLYSYTTDGNVTVTSSDGLWNNNTQFLFLEHSLLTANTTKGIYAGVCISVL 52
DB 249 PLYSYTTDGNVTVTSSDGLWNNNTQFLFLEHSLLTANTTKGIYAGVCISVL 300

RESULT 14
US-10-188-012-25
; Sequence 25, Application US/10188012
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Publication No. US20030124114A1
; GENERAL INFORMATION:
; APPLICANT: McIntire, Jennifer Jones
; APPLICANT: Umeteu, Dale T.
; APPLICANT: Dekruyff, Rosemarie
; APPLICANT: Kuchroo, Vijay
; APPLICANT: Freeman, Gordon J.
; TITLE OF INVENTION: T Cell Regulatory Genes and Methods of
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: STAN-235
; CURRENT APPLICATION NUMBER: US/10/188,012
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/302,344
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 364
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(364)
; OTHER INFORMATION: TIM-1 allele 5
US-10-188-012-25

Query Match      100.0%; Score 275; DB 14; Length 364;
Best Local Similarity 100.0%; Pred. No. 4.6e-28;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLYSYTTDGNVTVTSSDGLWNNNTQFLFLEHSLLTANTTKGIYAGVCISVL 52
DB 254 PLYSYTTDGNVTVTSSDGLWNNNTQFLFLEHSLLTANTTKGIYAGVCISVL 305

RESULT 15
US-10-663-497-25
; Sequence 25, Application US/10663497
; Publication No. US20050095593A1
; GENERAL INFORMATION:
; APPLICANT: Dale Umeteu
; APPLICANT: Rosemarie DeKruyff
; APPLICANT: Jennifer McIntire
; APPLICANT: Gordon Freeman
; TITLE OF INVENTION: T CELL REGULATORY GENES ASSOCIATED WITH
; TITLE OF INVENTION: IMMUNE DISEASE
; FILE REFERENCE: STAN-235CIP
; CURRENT APPLICATION NUMBER: US/10/663,497
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/302,344
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 10/188,012
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 364
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(364)
; OTHER INFORMATION: TIM-1 allele 5
US-10-663-497-25

Query Match      100.0%; Score 275; DB 17; Length 364;
Best Local Similarity 100.0%; Pred. No. 4.6e-28;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLYSYTTDGNVTVTSSDGLWNNNTQFLFLEHSLLTANTTKGIYAGVCISVL 52
DB 254 PLYSYTTDGNVTVTSSDGLWNNNTQFLFLEHSLLTANTTKGIYAGVCISVL 305
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Job time : 33.5894 secs

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OM protein - protein search, using sw model

Run on: June 29, 2005, 09:46:27 ; Search time 202.106 Seconds
(without alignments)
635.503 Million cell updates/sec

Title: US-10-718-321-7
Perfect score: 1749
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Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues
Total number of hits satisfying chosen parameters: 487488

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Maximum DB seq length: 50

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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 - 2: /cgn2_6/ptodata/1/pubpaa/PT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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 - 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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 - 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
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 - 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
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 - 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	98	5.6	35	15	US-10-434-269-23
3	81	4.6	41	15	US-10-057-783A-37
4	79	4.5	14	17	US-10-805-177-87
5	75	4.3	35	15	US-10-434-269-21
6	73	4.2	45	14	US-10-228-063-53
7	70.5	4.0	43	9	US-09-864-761-44813
8	70	4.0	12	17	US-10-805-177-88
9	67	3.8	12	17	US-10-805-177-92
10	67	3.8	34	9	US-09-916-494A-24
11	67	3.8	38	17	US-10-933-404-5
					Sequence 1, Appli
					Sequence 23, Appl
					Sequence 37, Appl
					Sequence 87, Appl
					Sequence 21, Appl
					Sequence 53, Appl
					Sequence 44813, A
					Sequence 88, Appl
					Sequence 92, Appl
					Sequence 24, Appl
					Sequence 5, Appli

12	66.5	3.8	37	17	US-10-935-254-45	Sequence 45, Appl
13	65	3.7	47	16	US-10-425-115-354965	Sequence 354965,
14	64	3.7	39	17	US-10-622-893A-10	Sequence 10, Appl
15	63	3.6	32	16	US-10-327-598-400	Sequence 40, Appl
16	63	3.6	47	13	US-10-105-934-17	Sequence 17, Appl
17	63	3.6	47	17	US-10-895-676-17	Sequence 17, Appl
18	62.5	3.6	40	16	US-10-425-115-352983	Sequence 352983,
19	62	3.5	34	9	US-09-864-761-37295	Sequence 37295, A
20	62	3.5	47	16	US-10-437-963-203485	Sequence 203485,
21	61.5	3.5	30	15	US-10-434-269-22	Sequence 22, Appl
22	61	3.5	34	17	US-10-933-404-6	Sequence 6, Appli
23	60.5	3.5	46	16	US-10-425-115-209986	Sequence 209986,
24	60	3.4	50	9	US-09-864-761-40317	Sequence 40317, A
25	59.5	3.4	45	9	US-09-864-761-39258	Sequence 39258, A
26	59.5	3.4	46	9	US-09-864-761-41678	Sequence 41678, A
27	59.5	3.4	48	9	US-09-799-514-18	Sequence 18, Appl
28	59	3.4	10	17	US-10-805-177-89	Sequence 89, Appl
29	59	3.4	15	17	US-10-718-321-5	Sequence 5, Appli
30	59	3.4	49	16	US-10-425-115-288406	Sequence 288406,
31	58	3.3	47	9	US-09-731-449-23	Sequence 22, Appl
32	58	3.3	47	9	US-09-731-449-23	Sequence 23, Appl
33	58	3.3	47	14	US-10-254-426-22	Sequence 22, Appl
34	58	3.3	47	14	US-10-254-426-23	Sequence 23, Appl
35	57	3.3	33	15	US-10-424-599-324859	Sequence 224859,
36	57	3.3	43	14	US-10-428-662-109	Sequence 109, App
37	57	3.3	44	15	US-10-424-599-189797	Sequence 189797,
38	57	3.3	45	15	US-10-424-599-258666	Sequence 258666,
39	56	3.2	10	17	US-10-805-177-93	Sequence 93, Appl
40	56	3.2	38	17	US-10-877-849-26	Sequence 26, Appl
41	56	3.2	45	16	US-10-425-115-288694	Sequence 288694,
42	56	3.2	47	16	US-10-425-115-195346	Sequence 195346,
43	56	3.2	50	17	US-10-492-403A-2	Sequence 2, Appli
44	55.5	3.2	40	10	US-09-798-889-84	Sequence 84, Appl
45	55.5	3.2	40	15	US-10-633-680-84	Sequence 84, Appl

ALIGNMENTS

RESULT 1
US-10-718-321-1
; Sequence 1, Application US/10718321
; Publication NO. US20050112117A1
; GENERAL INFORMATION:
; APPLICANT: Biogen Idec Ma Inc.
; APPLICANT: Bailly, Veronique
; APPLICANT: Bonventre, Joseph
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: Molecules and Methods for Inhibiting
; FILE REFERENCE: A124 US
; CURRENT APPLICATION NUMBER: US/10718,321
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/295449
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/295907
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US02/17402
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-718-321-1

Query Match 5.7%; Score 99; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 264 SSDGLWNNQTLFLEHS 281
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Db 1 SSDGLWNNQTLFLEHS 18

RESULT 2

US-10-434-269-23
; Sequence 23, Application US/10434269
; Publication No. US20040053296A1

; GENERAL INFORMATION:

; APPLICANT: ITO, Makoto, et al.

; TITLE OF INVENTION: A METHOD FOR TARGETING A POLYPEPTIDE ONTO CELLULAR SURFACE

; FILE REFERENCE: 1422-0588P

; CURRENT APPLICATION NUMBER: US/10/434,269

; CURRENT FILING DATE: 2003-05-09

; PRIOR APPLICATION NUMBER: US 10/434,269

; PRIOR FILING DATE: 2003-05-09

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 23

; LENGTH: 35

; TYPE: PRT

; ORGANISM: Insect intestinal mucin

US-10-434-269-23

Query Match 5.6%; Score 98; DB 15; Length 35;

Best Local Similarity 59.0%; Pred. No. 6.2;

Matches 23; Conservative 0; Mismatches 10; Indels 6; Gaps 2;

QY 152 TTTTVPVTTT-VPTTMSIPTTTTPTTMTVSTTTSVPTTT 189

||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 2 TTTQAPTTTQAPTTTQAPT---TTTQAPTTT 35

RESULT 3

US-10-057-783A-37

; Sequence 37, Application US/10057783A

; Publication No. US20040091955A1

; GENERAL INFORMATION:

; APPLICANT: Forster, Anthony C.

; TITLE OF INVENTION: Processes and compositions for peptide, protein and

; FILE REFERENCE: 1

; CURRENT APPLICATION NUMBER: US/10/057,783A

; CURRENT FILING DATE: 2002-01-25

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 37

; LENGTH: 41

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:FROM SYNTHETIC

; OTHER INFORMATION: DNA

US-10-057-783A-37

Query Match

Best Local Similarity 49.0%; Pred. No. 1.1e+02;

Matches 24; Conservative 2; Mismatches 13; Indels 10; Gaps 2;

QY 129 VTTTPIVTTVPTTVTRSTTVPTTTTPTTPTTMSIPTTTTPTT 177

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Db 2 VTTVVVTTTVTVTV---TTVVTVTVTVTV-----TWTVTTV 40

RESULT 4

US-10-805-177-87

; Sequence 87, Application US/10805177

; Publication No. US2005008449A1

; GENERAL INFORMATION:

; APPLICANT: Landes, Gregory M.

; APPLICANT: Chen, Francine

; APPLICANT: Bezabeh, Binyam

; APPLICANT: Foltz, Ian

; APPLICANT: Tse, Kam Fai

; APPLICANT: Jeffers, Michael
; APPLICANT: Mesri, Mehdi
; APPLICANT: Starling, Gary
; APPLICANT: Mezes, Peter
; APPLICANT: Khrantsov, Nikolai
; TITLE OF INVENTION: ANTIBODIES AGAINST T CELL IMMUNOGLOBULIN
; TITLE OF INVENTION: DOMAIN AND MUCIN DOMAIN 1 (TIM-1) ANTIGEN AND USES THEREOF
; FILE REFERENCE: ABXCUR.006A
; CURRENT APPLICATION NUMBER: US/10/805,177
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/456,652
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-805-177-87

Query Match 4.5%; Score 79; DB 17; Length 14;

Best Local Similarity 100.0%; Pred. No. 46;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 EMPPLPRQNHEPVAT 222

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Db 1 EMPPLPRQNHEPVAT 14

RESULT 5

US-10-434-269-21

; Sequence 21, Application US/10434269

; Publication No. US20040053296A1

; GENERAL INFORMATION:

; APPLICANT: ITO, Makoto, et al.

; TITLE OF INVENTION: A METHOD FOR TARGETING A POLYPEPTIDE ONTO CELLULAR SURFACE

; FILE REFERENCE: 1422-0588P

; CURRENT APPLICATION NUMBER: US/10/434,269

; CURRENT FILING DATE: 2003-05-09

; PRIOR APPLICATION NUMBER: US 10/434,269

; PRIOR FILING DATE: 2003-05-09

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 21

; LENGTH: 35

; TYPE: PRT

; ORGANISM: Rattus norvegicus

US-10-434-269-21

Query Match

Best Local Similarity 60.0%; Pred. No. 2.5e+02;

Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 174 PTTMTVSTTTSVPTTTSIPTTTSTVP 198

||||| : ||||| ||||| ||||| |||||

Db 2 PPTTSNSTPTSTPTSTPTSTPTSTP 26

RESULT 6

US-10-228-063-53

; Sequence 53, Application US/10228063

; Publication No. US20030135885A1

; GENERAL INFORMATION:

; APPLICANT: Lanahan, Mike

; TITLE OF INVENTION: Self-processing Plants and Plant Parts

; FILE REFERENCE: 109846.317

; CURRENT APPLICATION NUMBER: US/10/228,063

; CURRENT FILING DATE: 2002-12-12

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 53

; LENGTH: 45

; TYPE: PRT

Qy 147 STTVPTTTTVPVTTTVPVPTTMSIPTTTTVPPT-----MTVSTTTT 183

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Job time : 202.106 secs

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OM protein - protein search, using sw model

Run on: June 29, 2005, 09:33:11 ; Search time 60.3694 Seconds
(without alignments)
413.004 Million cell updates/sec

Title: US-10-718-321-7

Perfect score: 1749

Sequence: 1 MHPQVILSLHLADSVAG.....PFKKEVQQLRPHKSCIHORE 334

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 272444

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
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- 5: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	103	5.9	41	4	US-09-060-767B-5
2	86.5	4.9	41	4	US-09-060-767B-8
3	70.5	4.0	29	3	US-09-043-731-23
4	67	3.8	34	2	US-08-169-948B-24
5	67	3.8	34	2	US-08-448-873-24
6	67	3.8	34	3	US-08-382-452D-24
7	67	3.8	34	4	US-08-507-362A-12
8	67	3.8	34	4	US-09-516-494A-24
9	67	3.8	46	3	US-08-856-074A-39
10	64	3.7	25	4	US-09-060-767B-7
11	61.5	3.5	26	2	US-08-288-059-2
12	60.5	3.5	25	4	US-09-060-767B-4
13	59	3.4	40	2	US-08-530-569B-7
14	59	3.4	41	1	US-08-597-495B-28
15	59	3.4	41	3	US-09-068-051A-28
16	58	3.3	37	3	US-08-814-052-37
17	58	3.3	37	3	US-08-812-829-29
18	58	3.3	45	1	US-08-361-920-19
19	58	3.3	45	1	US-08-479-939-19
20	58	3.3	45	1	US-08-483-432-19
21	57	3.3	43	4	US-08-454-899G-109
22	55	3.1	45	1	US-08-451-947-98
23	55	3.1	45	2	US-08-424-826A-98
24	55	3.1	45	3	US-08-928-694-98
25	55	3.1	45	4	US-08-450-842-98
26	55	3.1	45	4	US-08-451-390-98
27	55	3.1	45	5	PCT-US91-06950-98

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28 54.5 3.1 43 2 US-08-169-948B-20 Sequence 20, Appl
29 54.5 3.1 43 2 US-08-448-873-20 Sequence 20, Appl
30 54.5 3.1 43 3 US-08-382-452D-20 Sequence 20, Appl
31 54.5 3.1 43 4 US-09-916-494A-20 Sequence 20, Appl
32 54.5 3.1 49 4 US-09-461-325-425 Sequence 425, App
33 54.5 3.1 49 4 US-10-012-542-425 Sequence 425, App
34 54.5 3.1 49 4 US-10-115-123-425 Sequence 425, App
35 53.5 3.1 45 4 US-09-270-767-35364 Sequence 35364, A
36 53.5 3.1 45 4 US-09-270-767-50581 Sequence 50581, A
37 53.5 3.1 50 5 PCT-US91-02942-9 Sequence 9, Appl
38 53 3.0 23 2 US-08-833-807-2 Sequence 2, Appl
39 53 3.0 23 2 US-09-223-043-2 Sequence 2, Appl
40 53 3.0 23 4 US-09-593-870A-2 Sequence 2, Appl
41 53 3.0 32 1 US-08-137-117D-132 Sequence 132, App
42 53 3.0 32 2 US-08-436-717-132 Sequence 132, App
43 53 3.0 44 3 US-08-955-937A-13 Sequence 13, Appl
44 53 3.0 44 3 US-09-300-985-13 Sequence 13, Appl
45 53 3.0 45 4 US-09-270-767-57229 Sequence 57229, A

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ALIGNMENTS

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RESULT 1
US-09-060-767B-5
; Sequence 5, Application US/09060767B
; Patent No. 6720152
; GENERAL INFORMATION:
; APPLICANT: Weil, Gary
; APPLICANT: Chandrashekar, Ramaswamy
; TITLE OF INVENTION: Diagnosis of Histoplasmosis Using Antigens Specific for
; FILE OF INVENTION: H. capsulatum
; FILE REFERENCE: BJCH 9986
; CURRENT APPLICATION NUMBER: US/09/060,767B
; CURRENT FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/043,332
; PRIOR FILING DATE: 1997-04-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Leishmania
US-09-060-767B-5

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Query Match          5.9%; Score 103; DB 4; Length 41;
Best Local Similarity 56.2%; Pred. No. 0.095; 10; Indels 8; Gaps 3;
Matches 27; Conservative 3; Mismatches 10; Indels 8; Gaps 3;

QY 151 PTTTTPVTPTTMSIPTTTTPTMTVSTTTSVPTTTSIPTTTSVP 198
Db      2 PTTTTPVTPTTMSIPTTTTPTMTVSTTTSVPTTTSIPTTTSVP 198

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RESULT 2
US-09-060-767B-8
; Sequence 8, Application US/09060767B
; Patent No. 6720152
; GENERAL INFORMATION:
; APPLICANT: Weil, Gary
; APPLICANT: Chandrashekar, Ramaswamy
; TITLE OF INVENTION: Diagnosis of Histoplasmosis Using Antigens Specific for
; FILE OF INVENTION: H. capsulatum
; FILE REFERENCE: BJCH 9986
; CURRENT APPLICATION NUMBER: US/09/060,767B
; CURRENT FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/043,332
; PRIOR FILING DATE: 1997-04-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 41
; TYPE: PRT

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; ORGANISM: Histoplasma Capsulatum
US-09-060-767B-8
Query Match 4.9%; Score 86.5; DB 4; Length 41;
Best Local Similarity 35.8%; Pred. NO. 2.1;
Matches 19; Conservative 8; Mismatches 11; Indels 15; Gaps 2;

QY 151 PTTTTPPTTPTTMSIPTTTPPTTMTVSTTTSVPTTTSIPTTTSVPTTIV 203
||||| ||||| ||||| ||||| :||| :||| :||| :||| :||| :|||
Db 2 PTTTPTTPTTPT-----PTTPTSI-----IPITPIVPANKIIVLTITII 39

RESULT 3
US-09-043-731-23
; Sequence 23, Application US/09043731A
; Patent No. 6344203
; GENERAL INFORMATION:
; APPLICANT: The Austin Research Institute
; TITLE OF INVENTION: Mimicking Peptides in Cancer Therapy
; FILE REFERENCE: CALA-200
; CURRENT APPLICATION NUMBER: US/09/043,731A
; CURRENT FILING DATE: 1998-06-23
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: single
; OTHER INFORMATION: stranded linear peptide
US-09-043-731-23

Query Match 4.0%; Score 70.5; DB 3; Length 29;
Best Local Similarity 57.1%; Pred. NO. 29;
Matches 16; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 168 PTTTTPPTTMTVSTTTSVPTTTSIPTTT 195
||||| :||| :||| :||| :||| :|||
Db 3 PTTTPTSTT-TWVPTPTPTGTQTPTTT 29

RESULT 4
US-08-169-948B-24
; Sequence 24, Application US/08169948B
; Patent No. 5861271
; GENERAL INFORMATION:
; APPLICANT: Fowler, Timothy
; APPLICANT: Ward, Michael
; APPLICANT: Clarkson, Kathleen
; APPLICANT: Collier, Katherine
; APPLICANT: Larenas, Edmund
; TITLE OF INVENTION: No. 5861271el Cellulase Enzymes and Systems
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 180 Kimball Way
; CITY: South San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/169,948B
; FILING DATE: DEC 17 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Horn, Margaret A.

; ORGANISM: Histoplasma Capsulatum
US-09-060-767B-8
Query Match 4.9%; Score 86.5; DB 4; Length 41;
Best Local Similarity 35.8%; Pred. NO. 2.1;
Matches 19; Conservative 8; Mismatches 11; Indels 15; Gaps 2;

QY 151 PTTTTPPTTPTTMSIPTTTPPTTMTVSTTTSVPTTTSIPTTTSVPTTIV 203
||||| ||||| ||||| ||||| :||| :||| :||| :||| :||| :|||
Db 2 PTTTPTTPTTPT-----PTTPTSI-----IPITPIVPANKIIVLTITII 39

RESULT 3
US-09-043-731-23
; Sequence 23, Application US/09043731A
; Patent No. 6344203
; GENERAL INFORMATION:
; APPLICANT: The Austin Research Institute
; TITLE OF INVENTION: Mimicking Peptides in Cancer Therapy
; FILE REFERENCE: CALA-200
; CURRENT APPLICATION NUMBER: US/09/043,731A
; CURRENT FILING DATE: 1998-06-23
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: single
; OTHER INFORMATION: stranded linear peptide
US-09-043-731-23

Query Match 4.0%; Score 70.5; DB 3; Length 29;
Best Local Similarity 57.1%; Pred. NO. 29;
Matches 16; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 168 PTTTTPPTTMTVSTTTSVPTTTSIPTTT 195
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Db 3 PTTTPTSTT-TWVPTPTPTGTQTPTTT 29

RESULT 4
US-08-169-948B-24
; Sequence 24, Application US/08169948B
; Patent No. 5861271
; GENERAL INFORMATION:
; APPLICANT: Fowler, Timothy
; APPLICANT: Ward, Michael
; APPLICANT: Clarkson, Kathleen
; APPLICANT: Collier, Katherine
; APPLICANT: Larenas, Edmund
; TITLE OF INVENTION: No. 5861271el Cellulase Enzymes and Systems
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 180 Kimball Way
; CITY: South San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/169,948B
; FILING DATE: DEC 17 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Horn, Margaret A.
```

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; REGISTRATION NUMBER: 33,401
; REFERENCE/DOCKET NUMBER: GC226
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 742-7536
; TELEFAX: (415) 742-7217
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-169-948B-24

Query Match 3.8%; Score 67; DB 2; Length 34;
Best Local Similarity 47.5%; Pred. NO. 68;
Matches 19; Conservative 5; Mismatches 10; Indels 6; Gaps 2;

QY 151 PTTTTPPTTPTTMSIPTTTPPTTMTVSTTTSVPTTTS 190
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Db 1 PGATTITSTRPP--SGPTTITRAT----STSSSTPTTSS 34

RESULT 5
US-08-448-873-24
; Sequence 24, Application US/08448873
; Patent No. 5874276
; GENERAL INFORMATION:
; APPLICANT: Fowler, Timothy
; APPLICANT: Ward, Michael
; APPLICANT: Clarkson, Kathleen
; APPLICANT: Collier, Katherine A.
; APPLICANT: Larenas, Edmund
; TITLE OF INVENTION: No. 5874276el Cellulase Enzymes and Systems
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 180 Kimball Way
; CITY: South San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,873
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/169,948
; FILING DATE: 17-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stone, Christopher L.
; REGISTRATION NUMBER: 35,696
; REFERENCE/DOCKET NUMBER: GC226D14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 742-7555
; TELEFAX: (415) 742-7217
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-448-873-24

Query Match 3.8%; Score 67; DB 2; Length 34;
Best Local Similarity 47.5%; Pred. NO. 68;
Matches 19; Conservative 5; Mismatches 10; Indels 6; Gaps 2;
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QY 151 PTTTTPPTTTTMSIPTTTTPTTMTVTSTTSVPTTTS 190
Db 1 PGATTITSTRPP--SGPTTITRAT-----STSSSTPTTSS 34

RESULT 6

US-08-382-452D-24
; Sequence 24, Application US/08382452D
; Patent No. 6268196
; GENERAL INFORMATION:
; APPLICANT: Fowler, Timothy
; APPLICANT: Clarkson, Kathleen A.
; APPLICANT: Ward, Michael
; APPLICANT: Collier, Katherine D.
; APPLICANT: Larenas, Edmund A.
; TITLE OF INVENTION: NOVEL CELLULOSE ENZYMES AND SYSTEMS
; TITLE OF INVENTION: FOR THEIR EXPRESSION
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/382,452D
; FILING DATE: February 1, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Christopher L. Stone
; REGISTRATION NUMBER: 36,696
; REFERENCE/DOCKET NUMBER: GC226-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 742-7217
; TELEFAX: (415) 742-7555
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-382-452D-24

Query Match 3.8%; Score 67; DB 3; Length 34;
Best Local Similarity 47.5%; Pred. No. 68;
Matches 19; Conservative 5; Mismatches 10; Indels 6; Gaps 2;

QY 151 PTTTTPPTTTTMSIPTTTTPTTMTVTSTTSVPTTTS 190
Db 1 PGATTITSTRPP--SGPTTITRAT-----STSSSTPTTSS 34

RESULT 7

US-08-507-362A-12
; Sequence 12, Application US/08507362A
; Patent No. 6562340
; GENERAL INFORMATION:
; APPLICANT: Bedford, Michael
; Morgan, Andrew
; Fowler, Timothy
; Ward, Michael
; Clarkson, Kathleen
; Collier, Katherine
; Larenas, Edmund
; TITLE OF INVENTION: An Enzyme Feed Additive and Animal Feed Including It
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International

; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/507,362A
; FILING DATE: 27-Oct-1995
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Castaneda, Janet
; REGISTRATION NUMBER: 33,228
; REFERENCE/DOCKET NUMBER: GC226-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 846-4072
; TELEFAX: (650) 845-6504
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-08-507-362A-12

Query Match 3.8%; Score 67; DB 4; Length 34;
Best Local Similarity 47.5%; Pred. No. 68;
Matches 19; Conservative 5; Mismatches 10; Indels 6; Gaps 2;

QY 151 PTTTTPPTTTTMSIPTTTTPTTMTVTSTTSVPTTTS 190
Db 1 PGATTITSTRPP--SGPTTITRAT-----STSSSTPTTSS 34

RESULT 8

US-09-916-494A-24
; Sequence 24, Application US/09916494A
; Patent No. 6620605
; GENERAL INFORMATION:
; APPLICANT: Fowler, Timothy
; APPLICANT: Clarkson, Kathleen A.
; APPLICANT: Ward, Michael
; APPLICANT: Collier, Katherine D.
; APPLICANT: Larenas, Edmund
; TITLE OF INVENTION: Method and Compositions for Treating
; TITLE OF INVENTION: Cellulose Containing Fabrics Using Truncated Cellulase
; TITLE OF INVENTION: Enzyme Compositions
; FILE REFERENCE: GC226-C4
; CURRENT APPLICATION NUMBER: US/09/916,494A
; CURRENT FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 08/382,452
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: US 08/169,948
; PRIOR FILING DATE: 1993-12-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Trichoderma longibrachiatum
US-09-916-494A-24

Query Match 3.8%; Score 67; DB 4; Length 34;
Best Local Similarity 47.5%; Pred. No. 68;
Matches 19; Conservative 5; Mismatches 10; Indels 6; Gaps 2;

QY 151 PTTTTPPTTTTMSIPTTTTPTTMTVTSTTSVPTTTS 190
Db 1 PGATTITSTRPP--SGPTTITRAT-----STSSSTPTTSS 34

Db 1 PGATTITSTRPP--SGPTTTTTRAT-----STSSSTPTTSS 34

RESULT 9

US-08-856-074A-39
; Sequence 39, Application US/08856074A
; Patent No. 6004798
; GENERAL INFORMATION:
; APPLICANT: Anderson, W. French
; APPLICANT: Wu, Bonnie W.
; TITLE OF INVENTION: Retroviral Envelopes Having
; TITLE OF INVENTION: Modified Hypervariable polyproline Regions
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,074A
; FILING DATE: 14-May-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 271010-378
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 973-994-1700
; TELEFAX: 973-994-1744
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
US-08-856-074A-39

Query Match 3.8%; Score 67; DB 3; Length 46;
Best Local Similarity 34.0%; Pred. No. 99;
Matches 16; Conservative 10; Mismatches 9; Indels 12; Gaps 2;

Qy 122 LEIVPPKVTTPITVTVTVTVTVTVTVTVTVTVTVTVTVTVTVTVTMSIP 168

Db 8 LEIVPAPQPPSPPLNTSYP-----PSTTSPTSTS-PTSPSPV 42

RESULT 10

US-09-060-767B-7
; Sequence 7, Application US/09060767B
; Patent No. 6720152
; GENERAL INFORMATION:
; APPLICANT: Weil, Gary
; APPLICANT: Chandrashekar, Ramaswamy
; TITLE OF INVENTION: Diagnosis of Histoplasmosis Using Antigens Specific for
; TITLE OF INVENTION: H. capsulatum
; FILE REFERENCE: BJCH 9986
; CURRENT APPLICATION NUMBER: US/09/060,767B
; CURRENT FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/043,332
; PRIOR FILING DATE: 1997-04-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 7
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Histoplasma Capsulatum
US-09-060-767B-7

Query Match 3.7%; Score 64; DB 4; Length 25;
Best Local Similarity 48.5%; Pred. No. 81;
Matches 16; Conservative 3; Mismatches 4; Indels 10; Gaps 2;

Qy 168 PTTTIVPTMTVSTTTSVPTTTSIPTTTSVPTT 200

Db 2 PTTT-----TTTTTPTPTPTSI-----IBIT 24

RESULT 11

US-08-288-059-2
; Sequence 2, Application US/08288059
; Patent No. 5827666
; GENERAL INFORMATION:
; APPLICANT: FINN, OLIVERA J.
; APPLICANT: FONTENOT, J. D.
; APPLICANT: MONTELARO, RONALD C.
; TITLE OF INVENTION: SYNTHETIC MULTIPLE TANDEM REPEAT MUCIN
; TITLE OF INVENTION: AND MUCIN-LIKE PEPTIDES, AND USES THEREOF
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/288,059
; FILING DATE: 08-AUG-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: CHAPIN, MAELANA K.
; REGISTRATION NUMBER: 35,843
; REFERENCE/DOCKET NUMBER: 61137/205204
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3711
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-288-059-2

Query Match 3.5%; Score 61.5; DB 2; Length 26;
Best Local Similarity 44.1%; Pred. No. 1.4e+02;
Matches 15; Conservative 1; Mismatches 9; Indels 9; Gaps 1;

Qy 130 TTTTIVPTVTVTVTVTSTTPTTPTTPTTPTTPTT 163

Db 2 TTTTPTT-----TTTPTPTPTPTPTPTTPTT 26

RESULT 12

US-09-060-767B-4
; Sequence 4, Application US/09060767B
; Patent No. 6720152
; GENERAL INFORMATION:

APPLICANT: Weil, Gary
APPLICANT: Chandrasekar, Ramaswamy
TITLE OF INVENTION: Diagnosis of Histoplasmosis Using Antigens Specific for
FILE OF INVENTION: H. capsulatum
FILE REFERENCE: BJCH 9986
CURRENT APPLICATION NUMBER: US/09/060,767B
CURRENT FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/043,332
PRIOR FILING DATE: 1997-04-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 25
TYPE: PRT
ORGANISM: Caldocellum saccharolyticum
US-09-060-767B-4

Query Match 3.5%; Score 60.5; DB 4; Length 25;
Best Local Similarity 52.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 10; Indels 1; Gaps 1;

QY 151 PTTTTPPTTPTTMSIPTTTTPT 175
DB 1 PTTTTPPTTPTTPTTPTTPTTPT 24

RESULT 13
US-08-530-569B-7
Sequence 7, Application US/08530569B
Patent No. 5939526
GENERAL INFORMATION:
APPLICANT: Gaugler, Beatrice
APPLICANT: van den Bynde, Benoit
APPLICANT: Schrier, Peter
APPLICANT: Brouwenstijn, Nathalie
APPLICANT: Boon-Fallieur, Thierry
TITLE OF INVENTION: Isolated RAGE-1 Derived Peptides Which
TITLE OF INVENTION: Complex with HLA-B7 Molecules and Uses Thereof
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: Federal Reserve Plaza, 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,569B
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: L0461/7002
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-530-569B-7

Query Match 3.4%; Score 59; DB 2; Length 40;
Best Local Similarity 42.9%; Pred. No. 3.8e+02;
Matches 12; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 186 PTTTSIPTTSPVPTTSTTFTVPPMLP 213
DB 6 PLRRSSPSSNRIRNTSTNNQFVPTMLP 33

RESULT 14
US-08-597-495B-28
Sequence 28, Application US/08597495B
Patent No. 5712369
GENERAL INFORMATION:
APPLICANT: Old, Lloyd J.; Welt, Sydney; Ritter, Gerd;
APPLICANT: Simpson, Richard J.; Nice, Edouard; Moritz, R. L.;
APPLICANT: Catimel, B.; Ji, Hong; Burgess, Anthony W.;
APPLICANT: Heath, Joan K.; White, Sara J.; Johnstone, Cameron
TITLE OF INVENTION: Colon Cell And Colon Cancer Cell
TITLE OF INVENTION: Associated Nucleic Acid Molecules, Protein And Peptides
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/597,495B
FILING DATE: 02-Feb-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/511,876
FILING DATE: 04-Aug-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5712369man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5316.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-597-495B-28

Query Match 3.4%; Score 59; DB 1; Length 41;
Best Local Similarity 29.4%; Pred. No. 3.9e+02;
Matches 10; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 74 DTRYKLLGLSRDVSLTIENTAVSDSGVYCCRV 107
DB 2 ENRVVSNDKESNASITIDQKTMDNGTYECV 35

RESULT 15
US-09-068-051A-28
Sequence 28, Application US/09068051A
Patent No. 6291235
GENERAL INFORMATION:
APPLICANT: Old, Lloyd J.; Welt, Sydney; Ritter, Gerd;
APPLICANT: Simpson, Richard J.; Nice, Edouard; Moritz, R. L.;
APPLICANT: Catimel, B.; Ji, Hong; Burgess, Anthony W.;
APPLICANT: Heath, Joan K.; White, Sara J.; Johnstone, Cameron
TITLE OF INVENTION: Colon Cell And Colon Cancer Cell
TITLE OF INVENTION: Associated Nucleic Acid Molecules, Protein And Peptides
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 29, 2005, 09:03:05 ; Search time 228.354 Seconds
(without alignments)
565.693 Million cell updates/sec

Title: US-10-718-321-7

Perfect score: 1749

Sequence: 1 MHPQVILSLIHLADSVAG.....PFKKEVQQLRPHKSCIHQRE 334

Scoring table: BLOSOM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 938430

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	5.8	18	AAO26686	Human KIM
2	99	5.7	18	AAO26687	Human KIM
3	99	5.7	18	AAO26673	Monoclonal
4	98	5.6	18	AAO26681	Human KIM
5	97	5.5	18	AAO26682	Human KIM
6	96.5	5.5	49	AAW59911	Amino aci
7	96	5.5	18	AAO26683	Human KIM
8	95	5.4	18	AAO26685	Human KIM
9	92	5.3	18	AAO26684	Human KIM
10	90	5.1	18	AAO26688	Human KIM
11	86.5	4.9	39	ABU53167	Human tes
12	79.5	4.5	34	ABU53169	Human tes
13	73	4.2	45	ABF96634	Raw-starc
14	71	4.1	38	AAW72130	Molecular
15	70.5	4.0	29	AAW21983	Human MUC
16	70.5	4.0	29	AAW22257	Muc pep 9
17	70.5	4.0	43	ABB41070	Peptide #
18	70.5	4.0	43	AAW34846	Peptide #
19	70.5	4.0	43	AAW74730	Human bon
20	70.5	4.0	43	AAW61928	Human bon
21	70.5	4.0	43	ABG56513	Human liv
22	70.5	4.0	43	ABG44533	Human pep
23	67	3.8	38	ADG14245	Cellulose
24	67	3.8	46	AAW88522	Amphotrop
25	65	3.7	48	AAO19219	Human sec

26	65	3.7	48	5	AAO19218	Human sec
27	64.5	3.7	39	3	AAG10258	Arabidops
28	63	3.6	32	7	ADM08777	Canine im
29	63	3.6	32	7	ADM08560	Canine im
30	62	3.5	34	4	AAW17640	Peptide #
31	62	3.5	34	4	ABB36660	Peptide #
32	62	3.5	34	4	AAW30158	Peptide #
33	62	3.5	34	4	ABB31447	Peptide #
34	62	3.5	34	4	ABB21997	Protein #
35	62	3.5	34	4	AAW69820	Human bon
36	62	3.5	34	4	AAW57424	Human bra
37	62	3.5	34	4	ABG51510	Human liv
38	62	3.5	34	4	AAW05299	Peptide #
39	62	3.5	34	5	ABG39446	Human pep
40	61.5	3.5	26	2	AAW72699	Human muc
41	61	3.5	34	7	ADG14246	Cellulose
42	60	3.4	39	4	ABU53259	Human tes
43	60	3.4	50	4	AAW20331	Peptide #
44	60	3.4	50	4	ABB40865	Peptide #
45	60	3.4	50	4	AAW34632	Peptide #

ALIGNMENTS

RESULT 1

AAO26686
ID AAO26686 standard; peptide; 18 AA.

XX AAO26686;

XX 20-MAR-2003 (first entry)

XX Human KIM-1 mucin domain related peptide, SEQ ID No 14.

XX Cytostatic; gene therapy; antibody; antigen; antigen-binding;
XX proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;
XX renal disease; injury; renal cancer.

XX Synthetic.

XX WO200298920-A1.

XX 12-DEC-2002.

XX 31-MAY-2002; 2002WO-US017402.

XX 01-JUN-2001; 2001US-0295449P.

XX 04-JUN-2001; 2001US-0295907P.

XX (BIOJ) BIOGEN INC.

XX (GEO) GEN HOSPITAL CORP.

XX Bailly V, Bonventre J;

XX WPI; 2003-156845/15.

XX New antibody, antibody derivative or antigen-binding polypeptide that
XX inhibits proteolytic release of a soluble kidney injury molecule-1
XX polypeptide, useful for treating or preventing renal disease or injury,
XX e.g. renal cancer.

XX Disclosure; Fig 1A; 42pp; English.

XX The invention relates to a novel antibody, antibody derivative or antigen
XX -binding polypeptide that inhibits proteolytic release of a soluble
XX kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.
XX The antibody, antibody derivative or antigen-binding polypeptide is
XX useful for treating or preventing renal disease or injury, e.g. renal
XX cancer. The antibody is also useful for inhibiting shedding of the KIM-1
XX polypeptide. This sequence represents a human KIM-1 mucin domain related
XX peptide of the invention

```

SQ Sequence 18 AA;
  Query Match          5.8%; Score 101; DB 6; Length 18;
  Best Local Similarity 100.0%; Pred. No. 1.4;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 TDGNDTVTSSDGLWNN 272
  |||||
Db 1 TDGNDTVTSSDGLWNN 18

RESULT 2
AAO26687
ID AAO26687 standard; peptide; 18 AA.
XX
AC AAO26687;
XX
DT 20-MAR-2003 (first entry)
XX
DE Human KIM-1 mucin domain related peptide, SEQ ID No 15.
XX
DE Cytostatic; gene therapy; antibody; antigen; antigen-binding;
KW proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;
KW renal disease; injury; renal cancer.
XX
OS Synthetic.
XX
PN WO200298920-A1.
XX
PD 12-DEC-2002.
XX
PF 31-MAY-2002; 2002WO-US017402.
XX
PR 01-JUN-2001; 2001US-0295449P.
XX
PR 04-JUN-2001; 2001US-0295907P.
XX
PA (BIOJ ) BIOGEN INC.
PA (GEHO ) GEN HOSPITAL CORP.
XX
PI Bailly V, Bonventre J;
XX
DR WPI; 2003-156845/15.
XX
PT New antibody, antibody derivative or antigen-binding polypeptide that
PT inhibits proteolytic release of a soluble kidney injury molecule-1
PT polypeptide, useful for treating or preventing renal disease or injury,
PT e.g. renal cancer.
XX
PS Claim 4; Page 25; 42pp; English.
XX
CC The invention relates to a novel antibody, antibody derivative or antigen
CC -binding polypeptide that inhibits proteolytic release of a soluble
CC kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.
CC The antibody, antibody derivative or antigen-binding polypeptide is
CC useful for treating or preventing renal disease or injury, e.g. renal
CC cancer. The antibody is also useful for inhibiting shedding of the KIM-1
CC polypeptide. This sequence represents a binding epitope of the invention
XX
SQ Sequence 18 AA;
  Query Match          5.7%; Score 99; DB 6; Length 18;
  Best Local Similarity 100.0%; Pred. No. 1.9;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 SSDGLWNNQTQLFLEHS 281
  |||||
Db 1 SSDGLWNNQTQLFLEHS 18

RESULT 4
AAO26681
ID AAO26681 standard; peptide; 18 AA.
XX
AC AAO26681;
XX
DT 20-MAR-2003 (first entry)
XX
DE Human KIM-1 mucin domain related peptide, SEQ ID No 9.
XX
DE Cytostatic; gene therapy; antibody; antigen; antigen-binding;
KW proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;
KW renal disease; injury; renal cancer.
XX
OS Synthetic.
XX
PN WO200298920-A1.
XX

```

```

PD 12-DEC-2002.
XX
PF 31-MAY-2002; 2002WO-US017402.
XX
PR 01-JUN-2001; 2001US-0295449P.
PR 04-JUN-2001; 2001US-0295907P.
XX
PA (BIOJ ) BIOGEN INC.
PA (GEO ) GEN HOSPITAL CORP.
XX
PI Bailly V, Bonventre J;
XX
DR WPI; 2003-156845/15.
XX
PT New antibody, antibody derivative or antigen-binding polypeptide that
PT inhibits proteolytic release of a soluble kidney injury molecule-1
PT polypeptide, useful for treating or preventing renal disease or injury,
PT e.g. renal cancer.
XX
PS Disclosure; Fig 1A; 42pp; English.
XX
CC The invention relates to a novel antibody, antibody derivative or antigen
CC -binding polypeptide that inhibits proteolytic release of a soluble
CC kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.
CC The antibody, antibody derivative or antigen-binding polypeptide is
CC useful for treating or preventing renal disease or injury, e.g. renal
CC cancer. The antibody is also useful for inhibiting shedding of the KIM-1
CC polypeptide. This sequence represents a human KIM-1 mucin domain related
XX peptide of the invention
XX
SQ Sequence 18 AA;
Query Match 5.5%; Score 97; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 PVATSPSPQPAETHPTT 236
DB 1 PVATSPSPQPAETHPTT 18

RESULT 6
AAW5911
ID AAW5911 standard; peptide; 49 AA.
XX
AC AAW5911;
XX
DT 20-NOV-1998 (first entry)
XX
DE Amino acid sequence of the mutanase enzyme PT box.
XX
KW Mutanase enzyme; PT box; alpha-1,3 glucoside bond; mutan; plaque;
KW bacteria; teeth.
XX
OS Bacillus sp.
XX
PN JP10201483-A.
XX
PD 04-AUG-1998.
XX
PF 01-OCT-1997; 97JP-00284362.
XX
PR 25-NOV-1996; 96JP-00314057.
XX (LIOY ) LION CORP.
XX
XX WPI; 1998-474495/41.
XX
PT Gene encoding a mutanase enzyme - used for prevention and removal of
PT plaque and bacteria on teeth.
XX
PS Claim 2; Page 5; 15pp; Japanese.
XX
CC This is the amino acid sequence of the mutanase enzyme PT box, which
CC decomposes the alpha-1,3 glucoside bond of mutan. The mutanase enzyme is
CC used in the method of the invention for prevention and removal of plaque
CC and bacteria on teeth
XX
SQ Sequence 49 AA;
Query Match 5.5%; Score 96.5; DB 2; Length 49;
Best Local Similarity 44.2%; Pred. No. 9.4;
Matches 23; Conservative 1; Mismatches 25; Indels 3; Gaps 1;

QY 147 STTVPTTTTPTTPTTMSIPTTTTPTTMTVTTTSVPTTTSPTTTSVP 198
DB 1 STSTPTPTPSPT---PTTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 49

```

```

PD 12-DEC-2002.
XX
PF 31-MAY-2002; 2002WO-US017402.
XX
PR 01-JUN-2001; 2001US-0295449P.
PR 04-JUN-2001; 2001US-0295907P.
XX
PA (BIOJ ) BIOGEN INC.
PA (GEO ) GEN HOSPITAL CORP.
XX
PI Bailly V, Bonventre J;
XX
DR WPI; 2003-156845/15.
XX
PT New antibody, antibody derivative or antigen-binding polypeptide that
PT inhibits proteolytic release of a soluble kidney injury molecule-1
PT polypeptide, useful for treating or preventing renal disease or injury,
PT e.g. renal cancer.
XX
PS Disclosure; Fig 1A; 42pp; English.
XX
CC The invention relates to a novel antibody, antibody derivative or antigen
CC -binding polypeptide that inhibits proteolytic release of a soluble
CC kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.
CC The antibody, antibody derivative or antigen-binding polypeptide is
CC useful for treating or preventing renal disease or injury, e.g. renal
CC cancer. The antibody is also useful for inhibiting shedding of the KIM-1
CC polypeptide. This sequence represents a human KIM-1 mucin domain related
XX peptide of the invention
XX
SQ Sequence 18 AA;
Query Match 5.6%; Score 98; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 210 MELPRQNHFPVATSPSP 227
DB 1 MELPRQNHFPVATSPSP 18

RESULT 5
AAO26682
ID AAO26682 standard; peptide; 18 AA.
XX
AC AAO26682;
XX
DT 20-MAR-2003 (first entry)
XX
DE Human KIM-1 mucin domain related peptide, SEQ ID No 10.
XX
KW Cytostatic; Gene therapy; antibody; antigen; antigen-binding;
KW proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;
KW renal disease; injury; renal cancer.
XX
OS Synthetic.
XX
PN WO200298920-A1.
XX
PD 12-DEC-2002.
XX
PF 31-MAY-2002; 2002WO-US017402.
XX
PR 01-JUN-2001; 2001US-0295449P.
PR 04-JUN-2001; 2001US-0295907P.
XX
PA (BIOJ ) BIOGEN INC.
PA (GEO ) GEN HOSPITAL CORP.
XX
PI Bailly V, Bonventre J;
XX
DR WPI; 2003-156845/15.
XX

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```

RESULT 7
AAO26683
ID AAO26683 standard; peptide; 18 AA.
XX
AC AAO26683;
XX
DT 20-MAR-2003 (first entry)
XX
DE Human KIM-1 mucin domain related peptide, SEQ ID No 11.
XX
KW Cytostatic; gene therapy; antibody; antigen; antigen-binding;
KW proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;
KW renal disease; injury; renal cancer.
XX
OS Synthetic.
XX
PN WO200298920-A1.
XX
PD 12-DEC-2002.
XX
PF 31-MAY-2002; 2002WO-US017402.
XX
PR 01-JUN-2001; 2001US-0295449P.
XX
PR 04-JUN-2001; 2001US-0295907P.
XX
PA (BIOJ ) BIOGEN INC.
PA (GEO ) GEN HOSPITAL CORP.
XX
PI Bailly V, Bonventre J;
XX
PI WPI; 2003-156845/15.
XX
PD 12-DEC-2002.
XX
PF 31-MAY-2002; 2002WO-US017402.
XX
PR 01-JUN-2001; 2001US-0295449P.
XX
PR 04-JUN-2001; 2001US-0295907P.
XX
PA (BIOJ ) BIOGEN INC.
PA (GEO ) GEN HOSPITAL CORP.
XX
PI Bailly V, Bonventre J;
XX
PI WPI; 2003-156845/15.
XX
PT New antibody, antibody derivative or antigen-binding polypeptide that
PT inhibits proteolytic release of a soluble kidney injury molecule-1
PT polypeptide, useful for treating or preventing renal disease or injury,
PT e.g. renal cancer.
XX
PS Disclosure; Fig 1A; 42pp; English.
XX
CC The invention relates to a novel antibody, antibody derivative or antigen
CC -binding polypeptide that inhibits proteolytic release of a soluble
CC kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.
CC The antibody, antibody derivative or antigen-binding polypeptide is
CC useful for treating or preventing renal disease or injury, e.g. renal
CC cancer. The antibody is also useful for inhibiting shedding of the KIM-1
CC polypeptide. This sequence represents a human KIM-1 mucin domain related
CC peptide of the invention
XX
SQ Sequence 18 AA;

Query Match 5.5%; Score 96; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 QPAETHPTTLOGAIRREP 245
DB 1 QPAETHPTTLOGAIRREP 18

RESULT 8
AAO26685
ID AAO26685 standard; peptide; 18 AA.
XX
AC AAO26685;
XX
DT 20-MAR-2003 (first entry)
XX
DE Human KIM-1 mucin domain related peptide, SEQ ID No 13.
XX
KW Cytostatic; gene therapy; antibody; antigen; antigen-binding;
KW proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;

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KW renal disease; injury; renal cancer.
XX
OS Synthetic.
XX
PN WO200298920-A1.
XX
PD 12-DEC-2002.
XX
PF 31-MAY-2002; 2002WO-US017402.
XX
PR 01-JUN-2001; 2001US-0295449P.
XX
PR 04-JUN-2001; 2001US-0295907P.
XX
PA (BIOJ ) BIOGEN INC.
PA (GEO ) GEN HOSPITAL CORP.
XX
PI Bailly V, Bonventre J;
XX
PI WPI; 2003-156845/15.
XX
PT New antibody, antibody derivative or antigen-binding polypeptide that
PT inhibits proteolytic release of a soluble kidney injury molecule-1
PT polypeptide, useful for treating or preventing renal disease or injury,
PT e.g. renal cancer.
XX
PS Disclosure; Fig 1A; 42pp; English.
XX
CC The invention relates to a novel antibody, antibody derivative or antigen
CC -binding polypeptide that inhibits proteolytic release of a soluble
CC kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.
CC The antibody, antibody derivative or antigen-binding polypeptide is
CC useful for treating or preventing renal disease or injury, e.g. renal
CC cancer. The antibody is also useful for inhibiting shedding of the KIM-1
CC polypeptide. This sequence represents a human KIM-1 mucin domain related
CC peptide of the invention
XX
SQ Sequence 18 AA;

Query Match 5.4%; Score 95; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 TSSPLYSYTTDGNDRVTE 263
DB 1 TSSPLYSYTTDGNDRVTE 18

RESULT 9
AAO26684
ID AAO26684 standard; peptide; 18 AA.
XX
AC AAO26684;
XX
DT 20-MAR-2003 (first entry)
XX
DE Human KIM-1 mucin domain related peptide, SEQ ID No 12.
XX
KW Cytostatic; gene therapy; antibody; antigen; antigen-binding;
KW proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;
KW renal disease; injury; renal cancer.
XX
OS Synthetic.
XX
PN WO200298920-A1.
XX
PD 12-DEC-2002.
XX
PF 31-MAY-2002; 2002WO-US017402.
XX
PR 01-JUN-2001; 2001US-0295449P.
XX
PR 04-JUN-2001; 2001US-0295907P.
XX
PA (BIOJ ) BIOGEN INC.

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PA (GEOH) GEN HOSPITAL CORP.
XX
PI Bailly V, Bonventre J;
XX
XX WPI; 2003-156845/15.
DR
XX New antibody, antibody derivative or antigen-binding polypeptide that
PT inhibits proteolytic release of a soluble kidney injury molecule-1
PT polypeptide, useful for treating or preventing renal disease or injury,
PT e.g. renal cancer.
XX
XX Disclosure; Fig 1A; 42pp; English.
XX
XX The invention relates to a novel antibody, antibody derivative or antigen
CC -binding polypeptide that inhibits proteolytic release of a soluble
CC kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.
CC The antibody, antibody derivative or antigen-binding polypeptide is
CC useful for treating or preventing renal disease or injury, e.g. renal
CC cancer. The antibody is also useful for inhibiting shedding of the KIM-1
CC polypeptide. This sequence represents a human KIM-1 mucin domain related
CC peptide of the invention
XX
XX Sequence 18 AA;
SQ

Query Match 5.3%; Score 92; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 237 LQAIRREPTSSPLSYT 254
DB 1 LQAIRREPTSSPLSYT 18

RESULT 10
AAO26688
ID AAO26688 standard; peptide; 18 AA.
XX
AC AAO26688;
XX
XX 20-MAR-2003 (first entry)
XX
XX Human KIM-1 mucin domain related peptide, SEQ ID No 16.
DE
XX Cytostatic; gene therapy; antibody; antigen; antigen-binding;
KW proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;
KW renal disease; injury; renal cancer.
XX
XX Synthetic.
OS
XX WO200298920-A1.
PN
XX 12-DEC-2002.
PD
XX
XX 31-MAY-2002; 2002WO-US017402.
PF
XX 01-JUN-2001; 2001US-0295449P.
PR
XX 04-JUN-2001; 2001US-0295907P.
PR
XX (BIOJ) BIOGEN INC.
PA
XX (GEOH) GEN HOSPITAL CORP.
PA
XX Bailly V, Bonventre J;
PI
XX WPI; 2003-156845/15.
DR
XX New antibody, antibody derivative or antigen-binding polypeptide that
PT inhibits proteolytic release of a soluble kidney injury molecule-1
PT polypeptide, useful for treating or preventing renal disease or injury,
PT e.g. renal cancer.
XX
XX Disclosure; Fig 1A; 42pp; English.
PS
XX The invention relates to a novel antibody, antibody derivative or antigen

CC -binding polypeptide that inhibits proteolytic release of a soluble
CC kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.
CC The antibody, antibody derivative or antigen-binding polypeptide is
CC useful for treating or preventing renal disease or injury, e.g. renal
CC cancer. The antibody is also useful for inhibiting shedding of the KIM-1
CC polypeptide. This sequence represents a human KIM-1 mucin domain related
CC peptide of the invention
XX
XX Sequence 18 AA;
SQ

Query Match 5.1%; Score 90; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 273 QTQLFLEHSLLTANTTKG 290
DB 1 QTQLFLEHSLLTANTTKG 18

RESULT 11
ABU53167
ID ABU53167 standard; protein; 39 AA.
XX
XX AC ABU53167;
XX
XX 14-APR-2003 (first entry)
DT
XX Human testes-derived DKFZphtes3_2a11 homologue #27.
DE
XX Human; gene therapy; vaccine; disease treatment; detection.
KW
XX Homo sapiens.
OS
XX WO200112659-A2.
PN
XX 22-FEB-2001.
PD
XX
XX 18-AUG-2000; 2000WO-IB001496.
PF
XX 18-AUG-1999; 99US-0149499P.
PR
XX 28-SEP-1999; 99US-0156503P.
PR
XX (GEHU-) GERMAN HUMAN GENOME PROJECT.
PA
XX Wiemann S;
PI
XX WPI; 2001-327840/34.
DR
XX Nucleic acids having the sequences of clones isolated from libraries of
PT different human tissues, useful in recombinant DNA methodologies.
PT
XX Example III; Page 776; 1095pp; English.
PS
XX This invention describes novel polynucleotides and polypeptides isolated
CC from human cDNA libraries which can be used for gene therapy or in
CC vaccines. The polynucleotides of the invention and antibodies encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate polypeptide expression. The products of the
CC invention may also be used to identify modulators of expression and
CC activity and to down regulate expression and activity. The antibodies of
CC the invention may also be used as diagnostic agents for detecting the
CC presence of polypeptides in samples. This sequence represents a homologue
CC of a polypeptide described in the disclosure of the invention
XX
XX Sequence 39 AA;
SQ

Query Match 4.9%; Score 86.5; DB 4; Length 39;
Best Local Similarity 55.0%; Pred. No. 38;
Matches 22; Conservative 5; Mismatches 10; Indels 3; Gaps 2;
QY 145 RIST-TVPTTTTPTTPTTMSIPTTTTPTTMTVSTTT 183
DB 1 RPTLTTLTTLPTT--PTSTTTTTTTTTSTVLSTT 38


```

PT  /note= "factor Xa cleavage recognition sequence"
PN  JP06277088-A.
XX
XX  04-OCT-1994.
PD
XX  30-MAR-1993; 93JP-00071559.
XX
XX  30-MAR-1993; 93JP-00071559.
PR
XX  (TOXS ) TOYO ENG CORP.
PA
XX  WPI; 1994-353764/44.
DR  N-PSDB; AAQ89357.
DR
XX  Prodn. and purificn. of recombinant protein without abnormal folding - by
PT  adding fused protein to transformed host organism and purifying fused
PT  protein by affinity chromatography using cellulose@ carrier.
XX
XX  Claim 2; Fig 3; 14pp; Japanese.
PS
XX  Recombinant proteins can be produced by affinity purification by
CC  utilising a molecular affinity tag. This sequence shows a molecular tag
CC  encoded by AAQ89357, and contains an endoglucinase III linker domain
CC  (EGIII LD) and a factor Xa cleavage recognition site. A nucleotide
CC  encoding a recombinant protein of interest can be inserted into a MCS
CC  (multiple cloning site), downstream of the cleavage site. The fused
CC  protein is purified when the EGIII LD is linked to an EGIII cellulose
CC  binding domain which binds to cellulose and affinity chromatography is
CC  carried out. The recombinant protein can then be recovered without the
CC  tag by cleavage using a specific protease, eg. factor Xa
XX
XX  Sequence 38 AA;
SQ
Query Match 4.1%; Score 71; DB 2; Length 38;
Best Local Similarity 48.8%; Pred. No. 4.8e+02;
Matches 20; Conservative 5; Mismatches 10; Indels 6; Gaps 2;

Qy 151 PTTTTPPTTPTMTSIPPTTMTVPTTMTVTTTSVPTTTSI 191
Db 1 PGTATTTSTRPP--SGPTTTTTRAT-----STSSSTPTTSSI 35

RESULT 15
AAW21983
ID AAW21983 standard; peptide; 29 AA.
XX
XX  AAW21983;
AC
XX  30-OCT-1997 (first entry)
XX
XX  Human MUC2 VNTR peptide Muc pep9.
DE
XX  Cancer; vaccine; peptide mimic; mucin; MUC2; Gal alpha(1,3)Gal;
KW  immunotherapy; therapy; adenocarcinoma; VNTR;
KW  variable number of tandem repeat.
XX
XX  Homo sapiens.
OS
XX  WO9711715-A1.
PN
XX  03-APR-1997.
PD
XX  27-SEP-1996; 96WO-AU000617.
PP
XX  27-SEP-1995; 95AU-00005680.
PR
XX  (AUST-) AUSTIN RES INST.
XX
XX  Sandrin MS, McKenzie IFC, Apostolopoulos V;
PI  WPI; 1997-212670/19.
XX
XX

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PT  Cancer vaccine containing MUC1 peptide mimic - used in the treatment of
PT  adenocarcinoma.
XX
XX  Example 1; Page 27; 55pp; English.
PS
XX
CC  Muc pep9 is a peptide derived from the variable number of tandem repeat
CC  (VNTR) region of human cancer mucin MUC2. Unlike other mucin VNTR-derived
CC  peptides (AAW21975-85), it is not capable of binding to anti-Gal
CC  alpha(1,3)Gal antibody. A novel cancer vaccine comprises a peptide
CC  (AAW21680-86) which mimics MUC1 or other cancer peptides and one or more
CC  pharmaceutically acceptable carrier or diluent, optionally in association
CC  with an appropriate carrier peptide or other therapeutic agent. Some
CC  mucin VNTR peptides (AAW21975-82) may also be used. The vaccine is used
CC  in the treatment of a patient suffering from, or with a predisposition
CC  to, adenocarcinoma (claimed)
XX
XX  Sequence 29 AA;
SQ
Query Match 4.0%; Score 70.5; DB 2; Length 29;
Best Local Similarity 57.1%; Pred. No. 3.8e+02;
Matches 16; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

Qy 168 PTTTTPPTTMTVSTTTSVPTTTSIPPTTT 195
Db 3 PTTTTPPTT-TMTVPTTPTPTGTPTTT 29

Search completed: June 29, 2005, 09:41:07
Job time : 230.354 secs

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OM protein - protein search, using sw model

Run on: June 29, 2005, 08:57:16 ; Search time 30.1847 Seconds
(without alignments)
1064.659 Million cell updates/sec

Title: US-10-718-321-7
Perfect score: 1749
Sequence: 1 MHPQVVLILHLADSVAG.....FPKKEVQQLRPHKSCIHORE 334
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1309	74.8	451	S71754	cellular hepatitis
2	260	14.9	770	T22808	hypothetical prote
3	246.5	14.1	662	A45155	mucin FIM-C.1 - Af
4	244	14.0	400	A28172	spasmolysin precu
5	242.5	13.9	851	T22696	hypothetical prote
6	234	13.4	371	S20075	promastigote surfa
7	229	13.1	216	I51920	mucin - rhesus mac
8	227.5	13.0	1832	T31113	mucin-like glycopor
9	221.5	12.7	3020	A43932	mucin 2 precursor,
10	219.5	12.6	327	S20074	promastigote surfa
11	216.5	12.4	294	A37232	mucin, tracheal (A
12	215	12.3	232	A60095	larval glue protei
13	214.5	12.3	235	PC2022	mucin like protein
14	213	12.2	167	A33532	mucin SMUC-40 - hu
15	212.5	12.1	307	GSF3	salivary glue prot
16	206	11.8	1161	S57180	probable membrane
17	205	11.7	447	A39321	mucin - rat (fragm
18	202.5	11.6	825	T29634	hypothetical prote
19	201.5	11.5	379	S50125	larval glue protei
20	201	11.5	660	JW0067	chitinase (EC 3.2.
21	200.5	11.5	1118	A48292	mucin, tracheobron
22	198	11.3	1513	A54895	mucin 2, intestina
23	195	11.1	345	E88103	protein W10G11.5 [
24	194	11.1	693	T19551	mucin-like protein
25	192.5	11.0	708	T19474	hypothetical prote
26	192.5	11.0	796	T21460	hypothetical prote
27	191	10.9	798	T34248	hypothetical prote
28	190.5	10.9	592	T34446	hypothetical prote
29	189.5	10.8	474	S15921	protein TPX-VT3 -

30	188.5	10.8	977	2	T16232	hypothetical prote
31	187.5	10.7	797	1	VBEX1	glycoprotein X pre
32	187.5	10.7	1235	2	T13710	protein-tyrosine k
33	186.5	10.7	292	2	S24169	mucin - rat
34	185.5	10.6	263	2	S01360	salivary glue prot
35	185	10.6	605	2	S48940	hypothetical prote
36	184	10.5	795	2	T20609	hypothetical prote
37	182.5	10.4	790	2	T34293	hypothetical prote
38	181.5	10.4	279	2	S53363	mucin SAC (clone J
39	181.5	10.4	602	2	AD2067	hypothetical prote
40	180	10.3	1777	2	T34369	hypothetical prote
41	179.5	10.3	921	2	AE0332	conserved hypotet
42	178	10.2	477	2	S53362	mucin SAC (clone J
43	177	10.1	560	2	T32661	hypothetical prote
44	175.5	10.0	217	2	S01358	salivary glue prot
45	175	10.0	866	2	T45462	membrane glycoprot

ALIGNMENTS

RESULT 1

S71754
cellular hepatitis A receptor HAVcr-1 precursor - green monkey
N:Alternate names: Surface Glycoprotein
C:Species: Cercopithecus aethiops (green monkey, grivet)
C:Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004
C:Accession: S71754
R:Kaplan, G.; Totsuka, A.; Thompson, P.; Akatsuka, T.; Moritsugu, Y.; Feinstone, S.M.
EMBO J. 15, 4282-4296, 1996
A:Title: Identification of a surface glycoprotein on African green monkey kidney cells as
A:Reference number: S71754; MUID:97015129; PMID:8861957
A:Accession: S71754
A:Molecule type: mRNA
A:Residues: 1-451 <KAP>
A:Cross-references: UNIPROT:Q95144; EMBL:X98252; NID:g1526573; PID:e247449; PID:g1526574
A:Experimental source: kidney
C:Keywords: Glycoprotein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-451/Product: cellular hepatitis A receptor HAVcr-1 #status predicted <MAT>

Query Match	74.8%	Score	1309;	DB	2;	Length	451;
Best Local Similarity	63.3%	Pred. No.	8.8e-74;				
Matches	255;	Conservative	36;	Mismatches	32;	Indels	80;
Gaps	3;						
Qy	1	MHPQVVLILHLADSVAGSVKVG3EAGPSVTLPCYSGAVTSMCNWRGSCSLFTCONG	60				
Db	1	MELQVVLILHLADSVADSVNDVGAGLSILPCRYNGAITSWNKRGTSVFCSPDG	60				
Qy	61	IWTNGTHVYRKOTRYKLLGDLRRDVSLLTIENTAVSDSGVYCCRVHRGFNDMKITV	120				
Db	61	IWTNGTHVYRKETRYKLLGNLSRRDVSLLTANTAVSDSGIYCCRVKHSWFNDMKITI	120				
Qy	121	SLEIVPPKV-----TTPIVTVTP	139				
Db	121	SLKIGPPRVTPIVRVRTSTVPTTTTLPTTLPTTLPTTLPTTLPTTLPTTLPTTLPT	180				
Qy	140	TVTVTSTVPTTTTTP-----TTVPTTMSIPTTTTPTTPTTPTTPTTPTTPTT	182				
Db	181	TTTVPPTTLPTTLPTTLPTTLPTTLPTTLPTTLPTTLPTTLPTTLPTTLPTTLPT	240				
Qy	183	T-----SVPTTSTIPTTTSVPVTTTSTVPTTPTTPTTPTTPTTPTTPTTPTT	220				
Db	241	TTLPPTTLPTTLPTTLPTTLPTTLPTTLPTTLPTTLPTTLPTTLPTTLPTTLPT	300				
Qy	221	ATSPSSPQPAETHPTLOGAIRREPTSSPLSYTTGDNPTVTESSDGLNNTQTLFLSH	280				
Db	301	ATSPSSPQPAETHPTVLLGATRTQPTSSPLSYTTGSDTPTVTESSDGLNNTQTLSPH	360				
Qy	281	SLLTANTTKGIYAGVCISVLVLLALLGVLIACKYFKKEVQOL	323				
Db	361	SPQMNTTEGIYAGVCISVLVLLALLGVLIACKYFKKEIQOL	403				

RESULT 5

T22696
hypothetical protein F5B11.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T22696
R:Ainscough, R.
submitted to the EMBL Data Library, December 1996
A/Reference number: Z19601
A/Accession: T22696
A>Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-851 <MIL>
A/Cross-references: UNIPROT:O17893; EMBL:Z83318; PIDN:CAB05903.1; GSPDB:GN00022; CESP:F5B11
A/Experimental source: clone F5B11
C:Genetics:
A/Gene: CESP.F5B11.3
A/Map position: 4
A/introns: 49/3; 123/3; 226/1; 282/3; 669/3; 743/3

	Query Match	Score 242.5; DB 2; Length 851;
	Best Local Similarity 46.8%; Pred. No. 1e-07;	
Matches	72; Conservative 15; Mismatches 48; Indels 19; Gaps 10;	
Qy	125 VPKVHTTP-IVTVPVVTV--RTSTVPTTT---RTSTVTP-TTMSIP-TTTTVPPT 176	
Dd	426 VT----- ----- ----- ----- ----- :: ---- ----- ----- ----- ----- ----- VTTTTTVPVTTTTTTSVTTTTTTSVTTTTTTSVTTTTTTSVTTTTTVPPT 485	
Qy	177 MTV--STTTSVTP-TTTSIP-TTTSVTP-VTTTSSVFVPPMPPLPRQNHEPVATSPSQPAE 231	
Dd	486 TTIVPPTTTSVPTTTPVPTTTPPTTTPPTTTPVPTTTPVPTTTPVPTTTPVPTTTPVS 539	
Qy	232 THPTTLOGAIRREPTSPLYTYTDGNDVTDESS 265	
Dd	540 TTTTIVPTTITVPTTTPVPTTTPVPTTTPVPTTTPVPTTTPVPTTTPVPTTTPVA 573	

RESULT 6

S20075
promastigote surface antigen P2 (clone 2.5) precursor - Leishmania major (fragment)
C:Species: Leishmania major
C/Date: 13-Jan-1995 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004
C/Accession: S20075; C41710
J:Murray, P.J.; Spithill, T.W.
J. Biol. Chem. 266, 24477-24484, 1991
A>Title: Variants of a Leishmania surface antigen derived from a multigenic family.
A/Reference number: A41710; UID:I92105105; PMID:1761547
A/Accession: S20075
A/Molecule type: mRNA
A/Residues: 1-371 <MUR>
C/Cross-references: UNIPROT:Q25333; EMBL:X57134; NID:G9580; PID:G9581
C/Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkage
F:1-343/Product: promastigote surface antigen P2 (fragment) #status predicted <PSA>
F:344-371/Domain: carboxyl-terminal propeptide #status predicted <CTR>
F:343/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asp) (in mature form)

	Query Match	Score 234; DB 2; Length 371;
	Best Local Similarity 29.3%; Pred. No. 1.4e-07;	
Matches	99; Conservative 28; Mismatches 127; Indels 84; Gaps 17;	
Qy	8 LSLIHLADSVAGSVKVGEGAPSVTLPHYSGAVTSMCNRGSCSFTCCNGIVWTNGT 67	
Dd	76 LMKVLRVLDD-DGSTVKCG-----TLPAE-----WSRMSTAAY-----FWLN-- 110	
Qy	68 HVTYRKDTRYKLGLDSRRDVSLLTIENTAVSDGSYGVCVRVEHGRFNFDKMKITVSLE ---- 123	
Dd	111 -----NYDLISLTLPPOWSSNPYL-R-GVSLKGRCFCGPESWANKADLAIEDKHK 161	
Qy	124 -----IYPKKVTHPIVTVTTRISTVTP-----TTTTVPTTVPPTMTSIP 168	
Dd	162 GSDCLAGKOCTTTTKLPTTTTTTKRPPTTT--TTTTKPPTTTTTTKPPTTTTTTKPPP 219	

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	228	82.9	451	2	S71754	cellular hepatitis
2	62.5	22.7	639	2	A48959	mitochondrial outer
3	62.5	22.7	1269	2	A90267	proteinase related
4	62	22.5	329	2	T18619	hypothetical prote
5	62	22.5	402	2	T29478	hypothetical prote
6	62	22.5	472	2	S36519	L2 protein - human
7	60	21.8	602	2	A45769	acetylcholine rece
8	59.5	21.6	103	1	CCBN	cytochrome c [vali
9	59.5	21.6	520	2	E86797	phage pi3 prote
10	59	21.5	846	2	C82135	chitinase VC1952 [
11	59	21.5	1254	1	JQ1978	structural polypro
12	58	21.1	321	2	T45053	hypothetical prote
13	58	21.1	639	2	A55019	muscarinic acetyl
14	58	21.1	1254	1	VHWVE	structural polypro
15	58	21.1	1254	1	VHWVT	structural polypro
16	58	21.1	1255	1	B44213	structural polypro
17	58	21.1	1355	1	D44213	structural polypro
18	57.5	20.9	405	2	H89930	protein R11G11.14
19	57.5	20.9	969	2	T17909	hypothetical prote
20	57	20.7	394	2	T18752	hypothetical prote
21	57	20.7	2399	2	H71879	toxin-like outer m
22	56.5	20.5	326	1	VGXRR	glycoprotein VP7 p
23	56.5	20.5	338	2	S75217	N-acetylglucosyl-L
24	56.5	20.5	775	2	A47311	polyprotein(C, E,
25	56.5	20.5	792	2	C32401	genome polyprotein
26	56.5	20.5	792	2	B32401	genome polyprotein
27	56.5	20.5	792	2	A32401	genome polyprotein
28	56.5	20.5	1226	1	GNWVP	genome polyprotein
29	56.5	20.5	1658	2	D86890	DNA-directed DNA p

C;Genetics:
A;Gene: SGD:TOM71; TOM72
A;Cross-references: SGD:S0001159; MIPS:YHR117w
A;Map position: 8R
A;Genome: nuclear
C;Superfamily: mitochondrial outer membrane protein, 70K; tetratricopeptide repeat homology <TT01>
C;Keywords: mitochondrial outer membrane; mitochondrion; transmembrane protein
F;86-119/Domain: tetratricopeptide repeat homology <TT01>
F;127-160/Domain: tetratricopeptide repeat homology <TT02>
F;161-194/Domain: tetratricopeptide repeat homology <TT03>
F;345-377/Domain: tetratricopeptide repeat homology #status atypical <TT04>
F;378-411/Domain: tetratricopeptide repeat homology <TT05>
F;412-445/Domain: tetratricopeptide repeat homology <TT06>
F;446-479/Domain: tetratricopeptide repeat homology <TT07>
F;480-513/Domain: tetratricopeptide repeat homology <TT08>
F;530-563/Domain: tetratricopeptide repeat homology <TT09>
F;564-597/Domain: tetratricopeptide repeat homology <TT10>

Query Match 22.7%; Score 62.5; DB 2; Length 639;
Best Local Similarity 40.5%; Pred. No.13;
Matches 17; Conservative 6; Mismatches 4; Indels 15; Gaps 2;

Qy 2 LYSVTTDG----NDVTETSSDGLWNNQTQLFLHLSLTANT 39
 ||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 305 LYSATDEGVLVANOLLTKSTD-----MYHLSLSTANT 335

RESULT 3
A90267
Proteinase related protein [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: A90267
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: A90267
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1269 <KUR>
A;Cross-references: UNIPROT:Q97206; GB:AEO06641; NID:g13814338; PIDN:AAK1392.1; GSPDB:G
C;Genetics:
A;Gene: SSO1141

Query Match	22.7%	Score 62.5;	DB 2;	Length 1269;
Best Local Similarity	29.2%;	Pred. No. 29;		
Matches	19;	Conservative 10;	Mismatches 19;	Indels 17; Gaps 2;
Qy	4	SYTTDG-----	NDVTTE-SSDGLWNNNQTLFLEHSLLTANTTKGIYAG	46
Db	1163	SFTTNGTHIVTINTQNYPDGGYNTLVTAIQSDGLSSSSVLYPENGTLNLTNKVNVISN		1222
Qy	47	VCISV	51	
		:	:	
Db	1223	OLTNV	1227	

```

RESULT 4
Tl8619
hypothetical protein AH6.10 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: Tl8619
R;Berks, M.
submitted to the EMBL Data Library, January 1995
A;Reference number: Z18998
A;Accession: Tl8619
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-329 <WIL>

```

A;Cross-references: UNIPROT:Q09208; EMBL:Z48009; PIDN:CRA88083.1; GSPDB:GN00020; CESP:AH6
A;Experimental source: clone AH6
C;Genetics:
A;Gene: CESP:AH6.10
A;Map position: 2
A;Introns: 217/2; 279/3
C;Superfamily: Caenorhabditis elegans hypothetical protein AH6.4

Query Match	22.5%	Score 62;	DB 2;	Length 329;
Best Local Similarity	43.8%	Pred. No. 7.2;		
Matches 14;	Conservative 5;	Mismatches 9;	Indels 4;	Gaps 1;

QY 25 QTQLFLEHSLTANTT---KGIYAGVCIISVL 52
| | | | | | | | | | | | | | | | | | | | | |
Db 119 QTGLLIERAFATFATYTKTKSVYIGVCISLI 150
| | | | | | | | | | | | | | | | | | | | | |

RESULT 5
T29478
hypothetical protein ZC487.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29478
R;Pauley, A.; Gattung, S.

A:Description: The sequence of *C. elegans* cosmid ZC487.
A:Reference: Reference number: Z20624
A:Accession: T29478
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-402 <PAU>
A:Cross-references: EMBL:Q23351; EMBL:U50310; PIDN:AAA92540.1; CESP:ZC487.1
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:ZC487.1
A:Introns: 7/2; 132/3; 165/3; 200/1; 244/3; 316/2
C:Superfamily: Caenorhabditis elegans hypothetical protein ZC487.1

	Query Match	22.58;	Score 62;	DB 2;	Length 402;	
	Best Local Similarity	30.9%;	Pred. No. 9.1;			
	Matches 21;	Conservative 9;	Mismatches 16;	Indels 22;	Gaps 4;	
Qy	5 YTTDGDN--TWTSSDGLWN-----NNQTQLFLBHSLLTANTTKGIYAGV	47				
Dd	181 YVDGHEFSAVCSSDGILGCISAIETHRSVLECIQNQPVALEY--LSANQTRDIFFGL	238				
Qy	48 ---CISVL 52					
Dd	239 ESFCIOVI 246					

RESULT 6
S36519
L2 protein - human papillomavirus type 34
C/Species: human papillomavirus type 34
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C/Accession: S36519
R/Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A/Description: Primer-directed sequencing of human papillomavirus types.
A/Reference number: S36469
A/Accession: S36519
A/Molecule type: DNA
A/Residues: 1-472
A/Cross-references: UNIPROT:P36758; EMBL:X74476; NID:G396989; PIDN:CAAS25595
C/Superfamily: papillomavirus L2 protein
C/Keywords: late protein

Query Match	22.5%	Score 62;	DB 2;	Length 472;
Best Local Similarity	37.0%	Pred. No. 11;		
Matches 17; Conservative	4;	Mismatches 25;	Indels 0;	Gaps 0;
Qv	2	LYSYTTGNDVTWTESSDGLNNTQTLFLEHSLLTANTTKGIYAGV	47	

DB 363 LYDVLDDNNVDITVEVPTGTNTQSVFASEISITTTANTTIFLNAGL 408

RESULT 7

A45769

acetylcholine receptor synthesis stimulator ARIA-1 precursor - chicken

C:Species: Gallus gallus (chicken)

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C:Accession: A45769

R: Falls, D.L.; Rosen, K.M.; Corfas, G.; Lane, W.S.; Fischbach, G.D.

Call 72, 801-815, 1993

A:Title: ARIA, a protein that stimulates acetylcholine receptor synthesis, is a member of

A:Reference number: A45769; MUID:93201602; PMID:8453670

A:Accession: A45769

A:Status: preliminary

A:Molecule type: mRNA; protein

A:Residues: 1-602 <PAL>

A:Cross-references: UNIPROT:Q05199; GB:L11264; NID:g212603; PIDN:AAA49037.1; PID:g212604

A:Experimental source: brain

A>Note: sequence extracted from NCBI backbone (NCBIN:127787, NCBIP:127788)

C:Superfamily: human heregulin; EGF homology; immunoglobulin homology

Query Match 21.8%; Score 60; DB 2; Length 602;

Best Local Similarity 31.7%; Pred. No. 25;

Matches 13; Conservative 11; Mismatches 15; Indels 2; Gaps 1;

QY 3 YSVTIDGNDTVTSSDGLNWNNOTOLF--EHSLLTANTTK 41

DB 301 YVSTTHSMTVTPTPSHSWSNGHTESILSRSHSVLVSSVE 341

RESULT 8

CCBN

cytochrome c [validated] - skipjack tuna

C:Species: Euthynnus pelamis, Katsuwonus pelamis (skipjack tuna)

C:Date: 13-Jul-1981 #sequence_revision 10-Oct-1997 #text_change 09-Jul-2004

C:Accession: A00022

R:Nakayama, T.; Titani, K.; Narita, K.

J. Biochem. 70, 311-326, 1971

A:Title: The amino acid sequence of cytochrome c from bonito (Katsuwonus pelamis, Linnae

A:Reference number: A00022; MUID:72003272; PMID:5106585

A:Accession: A00022

A:Molecule type: protein

A:Residues: 1-103 <NAK>

A:Cross-references: UNIPROT:P00025

R:Tanaka, N.; Yamane, T.; Tsukihara, T.; Ashida, T.; Kakudo, M.

submitted to the Brookhaven Protein Data Bank, August 1976

A:Reference number: A50107; PDB:1CVC

A:Contents: annotation; X-ray crystallography, reduced form, 2.3 angstroms

R:Tanaka, N.; Yamane, T.; Tsukihara, T.; Ashida, T.; Kakudo, M.

J. Biochem. 77, 147-162, 1975

A:Title: The crystal structure of bonito (katsuo) ferricytochrome c at 2.3 Å resolution.

A:Reference number: A38036; MUID:75170243; PMID:166072

A:Contents: annotation; X-ray crystallography, reduced form, 2.3 angstroms

R:Matsuura, Y.; Hata, Y.; Yamaguchi, T.; Tanaka, N.; Kakudo, M.

J. Biochem. 85, 729-737, 1979

A:Title: Structure of bonito heart ferricytochrome c and some remarks on molecular inter

A:Reference number: A38037; MUID:79150869; PMID:218921

A:Contents: annotation; X-ray crystallography, oxidized form, 2.8 angstroms

R:Mandel, N.; Mandel, G.; Trus, B.L.; Rosenberg, J.; Carlson, G.; Dickerson, R.E.

J. Biol. Chem. 252, 4619-4636, 1977

A:Title: Tuna cytochrome c at 2.0 Å resolution. III. Coordinate optimization and compari

A:Reference number: A38038; MUID:77207068; PMID:194885

A:Contents: annotation; commercial Scombridae, X-ray crystallography, oxidized and reduc

A>Note: this is the final paper in a series

C:Superfamily: cytochrome c; cytochrome c homology

C:Keywords: acetylated amino end; chromoprotein; electron transfer; heme; iron; metallo

F:4-98/Domain: cytochrome c homology <CYC>

F:1/Modified site: acetylated amino end (Gly) #status experimental

F:14,17/Binding site: heme (Cys) (covalent) #status experimental

F:18,80/Binding site: heme iron (His, Met) (axial ligands) #status experimental

Virology 152, 400-413, 1986
A:Title: Nucleotide sequence of the 26 S mRNA of the virulent Trinidad donkey strain of
A:Reference number: A47612; MUID:86263392; PMID:3088830
A:Accession: A47612
A:Molecule type: mRNA
A:Residues: 1-542,'K',544-810,'P',812-1254 <K12>
A:Cross-references: GB:L01442
C:Superfamily: togavirus structural polypeptide
F:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-275/Product: coat protein #status predicted <CTP>
F:276-334/Product: membrane glycoprotein E3 #status predicted <MG3>
F:335-757/Product: membrane glycoprotein E2 #status predicted <MG2>
F:701-718/Domain: transmembrane #status predicted <TM1>
F:758-812/Product: sK protein #status predicted <KP6>
F:774-790/Domain: transmembrane #status predicted <TM2>
F:795-813/Domain: transmembrane #status predicted <TM3>
F:813-1254/Product: membrane glycoprotein E1 #status predicted <MG1>
F:1231-1248/Domain: transmembrane #status predicted <TM4>
F:47,286,546,652,946/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 21.1%; Score 58; DB 1; Length 1254;
Best Local Similarity 47.6%; Pred. No. 1e+02;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 11 DTVTSSDGLWNNQQLFLE 31
DB 758 ETTWESLDHLWNNNQMFMIQ 778

Search completed: June 29, 2005, 08:58:15
Job time : 5.69941 secs

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GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 29, 2005, 08:58:20 ; Search time 209.324 Seconds
(without alignments)
613.589 Million cell updates/sec

Title: US-10-718-321-7
Perfect score: 1749
Sequence: 1 MHPQVILSLIHLADSVAG.....PFKKEVQQLRPHKSCIHORE 334

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PT_NEW_PUB.pep.*
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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
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9: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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14: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10F_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1749	100.0	334	17	US-10-655-506-7
2	1749	100.0	334	17	US-10-718-321-7
3	1684	96.3	359	14	US-10-188-012-17
4	1684	96.3	359	15	US-10-295-027-302
5	1684	96.3	359	15	US-10-188-832-64
6	1684	96.3	359	17	US-10-391-939A-4
7	1684	96.3	359	17	US-10-663-497-17
8	1684	96.3	359	17	US-10-718-321-8
9	1684	96.3	359	17	US-10-847-918-25
10	1679	96.0	359	14	US-10-188-012-19
11	1679	96.0	359	17	US-10-663-497-19
					Sequence 7, Appli
					Sequence 7, Appli
					Sequence 17, Appl
					Sequence 302, App
					Sequence 64, Appl
					Sequence 4, Appli
					Sequence 17, Appl
					Sequence 8, Appli
					Sequence 25, Appl
					Sequence 19, Appl

12 1671 95.5 359 14 US-10-188-012-23 Sequence 23, Appli
13 1671 95.5 359 17 US-10-663-497-23 Sequence 23, Appli
14 1666 95.3 365 14 US-10-188-012-21 Sequence 21, Appl
15 1666 95.3 365 17 US-10-663-497-21 Sequence 21, Appl
16 1655.5 94.7 364 14 US-10-188-012-25 Sequence 25, Appl
17 1655.5 94.7 364 17 US-10-663-497-25 Sequence 25, Appl
18 1643.5 94.0 364 14 US-10-188-012-27 Sequence 27, Appl
19 1643.5 94.0 364 17 US-10-663-497-27 Sequence 27, Appl
20 1587 90.7 339 17 US-10-391-939A-2 Sequence 2, Appli
21 1587 90.7 339 17 US-10-391-939A-28 Sequence 28, Appli
22 1393 79.6 263 17 US-10-391-939A-6 Sequence 6, Appli
23 1393 79.6 263 17 US-10-391-939A-32 Sequence 32, Appli
24 1393 79.6 263 17 US-10-391-939A-39 Sequence 39, Appli
25 1393 79.6 263 17 US-10-391-939A-8 Sequence 50, Appli
26 592 33.8 108 17 US-10-805-177-50 Sequence 8, Appli
27 522.5 29.9 307 17 US-10-655-506-3 Sequence 3, Appli
28 519 29.7 305 14 US-10-188-012-1 Sequence 1, Appli
29 519 29.7 305 17 US-10-663-497-1 Sequence 1, Appli
30 491.5 28.1 282 14 US-10-188-012-3 Sequence 3, Appli
31 491.5 28.1 282 17 US-10-663-497-3 Sequence 3, Appli
32 432 24.7 81 17 US-10-718-321-6 Sequence 6, Appli
33 405 23.2 345 14 US-10-188-012-13 Sequence 13, Appli
34 405 23.2 345 17 US-10-663-497-13 Sequence 13, Appli
35 401 22.9 305 14 US-10-188-012-5 Sequence 5, Appli
36 401 22.9 305 14 US-10-188-012-7 Sequence 7, Appli
37 401 22.9 305 17 US-10-663-497-5 Sequence 5, Appli
38 401 22.9 305 17 US-10-663-497-7 Sequence 7, Appli
39 401 22.9 345 14 US-10-188-012-15 Sequence 15, Appli
40 401 22.9 345 17 US-10-663-497-15 Sequence 15, Appli
41 367.5 21.0 378 14 US-10-188-012-33 Sequence 33, Appli
42 367.5 21.0 378 17 US-10-663-497-33 Sequence 33, Appli
43 367.5 21.0 379 10 US-09-813-153-138 Sequence 138, App
44 366.5 21.0 378 14 US-10-188-012-35 Sequence 35, Appli
45 366.5 21.0 378 17 US-10-663-497-35 Sequence 35, Appli

ALIGNMENTS

RESULT 1

US-10-655-506-7
/ Sequence 7, Application US/10655506
/ Publication No. US2005008986A1
/ GENERAL INFORMATION:
/ APPLICANT: Michele Sanicola-Nadel
/ Joseph V. Bonventre
/ Catherine A. Heesion
/ Takaharu Ichimura
/ Henry Wei
/ Richard L. Cate
/ TITLE OF INVENTION: MODULATORS OF TISSUE REGENERATION
/ NUMBER OF SEQUENCES: 7
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Biogen, Inc.
/ STREET: 14 Cambridge Center
/ CITY: Cambridge
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02142
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION NUMBER: US/10/655,506
/ FILING DATE: 04-Sep-2003
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/197,970
/ FILING DATE: 23-Nov-1998
/ APPLICATION NUMBER: US 60/018,228
/ FILING DATE: 24-MAY-1996

```
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Levine, Leslie M.
; REGISTRATION NUMBER: 35,245
; REFERENCE/DOCKET NUMBER: A010 PCT CIP-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 679-2810
; TELEFAX: (617) 679-2838
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 334 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-655-506-7

Query Match      100.0%; Score 1749; DB 17; Length 334;
Best Local Similarity 100.0%; Pred. No. 1.5e-113;
Matches 334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHPQVILSLHLADSVAGSVKVGGEAGPSVTLPCHYSGAVTSMCWNRGSCSLFTCQNG 60
DB 1 MHPQVILSLHLADSVAGSVKVGGEAGPSVTLPCHYSGAVTSMCWNRGSCSLFTCQNG 60
QY 61 IWWTNGTHVTRKOTRYKLLGDLSDRDVSLTIENTAVSDSGVCCRVHRGFNDMKITV 120
DB 61 IWWTNGTHVTRKOTRYKLLGDLSDRDVSLTIENTAVSDSGVCCRVHRGFNDMKITV 120
QY 121 SLEIVPPKVTTPITVTPTVTTRTSTTPTPTTPTTPTTPTTPTTPTTPTTPTTPTT 180
DB 121 SLEIVPPKVTTPITVTPTVTTRTSTTPTPTTPTTPTTPTTPTTPTTPTTPTTPTT 180
QY 181 TTTSVPTTTSIPTTTSVPVTTVTVTFVPPMPLPRQNHPEPVATSPSPQPAETHPTTLOGA 240
DB 181 TTTSVPTTTSIPTTTSVPVTTVTVTFVPPMPLPRQNHPEPVATSPSPQPAETHPTTLOGA 240
QY 241 IRREPTSSPLSYTTDGDNDVTETSSDGLWNNNOTQLFLEHSLLTANTTKGIYAGVCISVL 300
DB 241 IRREPTSSPLSYTTDGDNDVTETSSDGLWNNNOTQLFLEHSLLTANTTKGIYAGVCISVL 300
QY 301 VLLALLGVIIIAKKYFFKKEVQQLRPHKSCIHORE 334
DB 301 VLLALLGVIIIAKKYFFKKEVQQLRPHKSCIHORE 334

RESULT 3
US-10-188-012-17
; Sequence 17, Application US/10188012
; Publication No. US20030124114A1
; GENERAL INFORMATION:
; APPLICANT: McIntire, Jennifer Jones
; APPLICANT: Umetsu, Dale T.
; APPLICANT: Dekruyff, Rosemarie
; APPLICANT: Kuchroo, Vijay
; APPLICANT: Freeman, Gordon J.
; TITLE OF INVENTION: T Cell Regulatory Genes and Methods of
; FILE OF INVENTION: Use Thereof
; CURRENT APPLICATION NUMBER: US/10188,012
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/302,344
; FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 359
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(360)
; OTHER INFORMATION: TIM-1 allele 1
US-10-188-012-17

Query Match      96.3%; Score 1684; DB 14; Length 359;
Best Local Similarity 100.0%; Pred. No. 5.2e-109;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHPQVILSLHLADSVAGSVKVGGEAGPSVTLPCHYSGAVTSMCWNRGSCSLFTCQNG 60
DB 1 MHPQVILSLHLADSVAGSVKVGGEAGPSVTLPCHYSGAVTSMCWNRGSCSLFTCQNG 60
QY 61 IWWTNGTHVTRKOTRYKLLGDLSDRDVSLTIENTAVSDSGVCCRVHRGFNDMKITV 120
DB 61 IWWTNGTHVTRKOTRYKLLGDLSDRDVSLTIENTAVSDSGVCCRVHRGFNDMKITV 120
QY 121 SLEIVPPKVTTPITVTPTVTTRTSTTPTPTTPTTPTTPTTPTTPTTPTTPTTPTT 180
DB 121 SLEIVPPKVTTPITVTPTVTTRTSTTPTPTTPTTPTTPTTPTTPTTPTTPTTPTT 180

;
; ATTORNEY/AGENT INFORMATION:
; NAME: Levine, Leslie M.
; REGISTRATION NUMBER: 35,245
; REFERENCE/DOCKET NUMBER: A010 PCT CIP-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 679-2810
; TELEFAX: (617) 679-2838
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 334 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-655-506-7

Query Match      100.0%; Score 1749; DB 17; Length 334;
Best Local Similarity 100.0%; Pred. No. 1.5e-113;
Matches 334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHPQVILSLHLADSVAGSVKVGGEAGPSVTLPCHYSGAVTSMCWNRGSCSLFTCQNG 60
DB 1 MHPQVILSLHLADSVAGSVKVGGEAGPSVTLPCHYSGAVTSMCWNRGSCSLFTCQNG 60
QY 61 IWWTNGTHVTRKOTRYKLLGDLSDRDVSLTIENTAVSDSGVCCRVHRGFNDMKITV 120
DB 61 IWWTNGTHVTRKOTRYKLLGDLSDRDVSLTIENTAVSDSGVCCRVHRGFNDMKITV 120
QY 121 SLEIVPPKVTTPITVTPTVTTRTSTTPTPTTPTTPTTPTTPTTPTTPTTPTTPTT 180
DB 121 SLEIVPPKVTTPITVTPTVTTRTSTTPTPTTPTTPTTPTTPTTPTTPTTPTTPTT 180
QY 181 TTTSVPTTTSIPTTTSVPVTTVTVTFVPPMPLPRQNHPEPVATSPSPQPAETHPTTLOGA 240
DB 181 TTTSVPTTTSIPTTTSVPVTTVTVTFVPPMPLPRQNHPEPVATSPSPQPAETHPTTLOGA 240
QY 241 IRREPTSSPLSYTTDGDNDVTETSSDGLWNNNOTQLFLEHSLLTANTTKGIYAGVCISVL 300
DB 241 IRREPTSSPLSYTTDGDNDVTETSSDGLWNNNOTQLFLEHSLLTANTTKGIYAGVCISVL 300
QY 301 VLLALLGVIIIAKKYFFKKEVQQLRPHKSCIHORE 334
DB 301 VLLALLGVIIIAKKYFFKKEVQQLRPHKSCIHORE 334

RESULT 2
US-10-718-321-7
; Sequence 7, Application US/10718321
; Publication No. US20050112117A1
; GENERAL INFORMATION:
; APPLICANT: Biogen Idec Ma Inc.
; APPLICANT: Bailly, Veronique
; APPLICANT: Bonventre, Joseph
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: Molecules and Methods for Inhibiting
; FILE OF INVENTION: Shedding of KIM-1
; FILE REFERENCE: A124 US
; CURRENT APPLICATION NUMBER: US/10/718,321
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/295449
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/295907
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US02/17402
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-718-321-7
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; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-718-321-8

Query Match      96.3%; Score 1684; DB 17; Length 359;
Best Local Similarity 100.0%; Pred. No. 5.2e-109;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHPQVILSLIHLADSVAGSVKVGEGAPSVTLPCHYSGAVTSMCNRGSCSLFTCCQNG 60
DB 1 MHPQVILSLIHLADSVAGSVKVGEGAPSVTLPCHYSGAVTSMCNRGSCSLFTCCQNG 60
QY 61 IVWTNGTHVTRKDYKLLGLDLSRDDVSLTIENTAVSDSGVYCCRVHRGFNDMKITV 120
DB 61 IVWTNGTHVTRKDYKLLGLDLSRDDVSLTIENTAVSDSGVYCCRVHRGFNDMKITV 120
QY 121 SLEIVPPKVTTPITVTTVTTRTSITVPTTTTPTTPTTPTTPTTPTTPTTPTTPTT 180
DB 121 SLEIVPPKVTTPITVTTVTTRTSITVPTTTTPTTPTTPTTPTTPTTPTTPTTPTT 180
QY 181 TTTSVPTTTSIPTTTSVPVTTTSTVFVPPMPLPRQNHPEPVATSPSPQPAETHPTTLOGA 240
DB 181 TTTSVPTTTSIPTTTSVPVTTTSTVFVPPMPLPRQNHPEPVATSPSPQPAETHPTTLOGA 240
QY 241 IRREPTSSPLSYTTDGNDDVTSSDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 300
DB 241 IRREPTSSPLSYTTDGNDDVTSSDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 300
QY 301 VLLALLGVIIIAKKYFFKKEVQQL 323
DB 301 VLLALLGVIIIAKKYFFKKEVQQL 323

RESULT 9
US-10-847-918-25
; Sequence 25, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-847-918-25

Query Match      96.3%; Score 1684; DB 17; Length 359;
Best Local Similarity 100.0%; Pred. No. 5.2e-109;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHPQVILSLIHLADSVAGSVKVGEGAPSVTLPCHYSGAVTSMCNRGSCSLFTCCQNG 60
DB 1 MHPQVILSLIHLADSVAGSVKVGEGAPSVTLPCHYSGAVTSMCNRGSCSLFTCCQNG 60
QY 61 IVWTNGTHVTRKDYKLLGLDLSRDDVSLTIENTAVSDSGVYCCRVHRGFNDMKITV 120
DB 61 IVWTNGTHVTRKDYKLLGLDLSRDDVSLTIENTAVSDSGVYCCRVHRGFNDMKITV 120

Query Match      96.0%; Score 1679; DB 14; Length 359;
Best Local Similarity 99.7%; Pred. No. 1.2e-108;
Matches 322; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MHPQVILSLIHLADSVAGSVKVGEGAPSVTLPCHYSGAVTSMCNRGSCSLFTCCQNG 60
DB 1 MHPQVILSLIHLADSVAGSVKVGEGAPSVTLPCHYSGAVTSMCNRGSCSLFTCCQNG 60
QY 61 IVWTNGTHVTRKDYKLLGLDLSRDDVSLTIENTAVSDSGVYCCRVHRGFNDMKITV 120
DB 61 IVWTNGTHVTRKDYKLLGLDLSRDDVSLTIENTAVSDSGVYCCRVHRGFNDMKITV 120
QY 121 SLEIVPPKVTTPITVTTVTTRTSITVPTTTTPTTPTTPTTPTTPTTPTTPTTPTT 180
DB 121 SLEIVPPKVTTPITVTTVTTRTSITVPTTTTPTTPTTPTTPTTPTTPTTPTTPTT 180
QY 181 TTTSVPTTTSIPTTTSVPVTTTSTVFVPPMPLPRQNHPEPVATSPSPQPAETHPTTLOGA 240
DB 181 TTTSVPTTTSIPTTTSVPVTTTSTVFVPPMPLPRQNHPEPVATSPSPQPAETHPTTLOGA 240
QY 241 IRREPTSSPLSYTTDGNDDVTSSDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 300
DB 241 IRREPTSSPLSYTTDGNDDVTSSDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 300
QY 301 VLLALLGVIIIAKKYFFKKEVQQL 323
DB 301 VLLALLGVIIIAKKYFFKKEVQQL 323

RESULT 10
US-10-188-012-19
; Sequence 19, Application US/10188012
; Publication No. US20030124114A1
; GENERAL INFORMATION:
; APPLICANT: McIntire, Jennifer Jones
; APPLICANT: Umetsu, Dale T.
; APPLICANT: Dekruyff, Rosemarie
; APPLICANT: Kuchroo, Vijay
; APPLICANT: Freeman, Gordon J.
; TITLE OF INVENTION: T Cell Regulatory Genes and Methods of
; FILE REFERENCE: STAN-235
; CURRENT APPLICATION NUMBER: US/10/188,012
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/302,344
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 359
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(359)
; OTHER INFORMATION: TIM-1, allele 2
US-10-188-012-19
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; LOCATION: (1)...(359)
; OTHER INFORMATION: TIM-1, allele 4
US-10-663-497-23

Query Match          95.5%; Score 1671; DB 17; Length 359;
Best Local Similarity 99.1%; Pred. No. 4.2e-108;
Matches 320; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MHPQVILSLIHLADSVAGSVKVGEGAPSVTLPCYSGAVTSMCMNRGSCSLFTCQNG 60
DB 1 MHPQVILSLIHLADSVAGSVKVGEGAPSVTLPCYSGAVTSMCMNRGSCSLFTCQNG 60
QY 61 IWWTNGTHVTKDTRYKLLGLDLSRDDVSLTIENTAVSDSGVYCCRVHRGFNDMKITV 120
DB 61 IWWTNGTHVTKDTRYKLLGLDLSRDDVSLTIENTAVSDSGVYCCRVHRGFNDMKITV 120
QY 121 SLEIVPPKVTTPPIVTTVPTVTRTSTVPTTTTTPVTTPVTTPVTTPVTTPVTTP 180
DB 121 SLEIVPPKVTTPPIVTTVPTVTRTSTVPTTTTTPVTTPVTTPVTTPVTTPVTTP 180
QY 181 TTTSVPTTTSIPTTTSVPVTTVPFVPPMPLPRQNHPEVATSPSPQPAETHPTLQGT 240
DB 181 TTTSVPTTTSIPTTTSVPVTTVPFVPPMPLPRQNHPEVATSPSPQPAETHPTLQGT 240
QY 241 IRREPTSPSYTTDNDVTVESSDGLMNNQTLFLEHSLLTANTTKGIYAGVCISVL 300
DB 241 IRREPTSPSYTTDNDVTVESSDGLMNNQTLFLEHSLLTANTTKGIYAGVCISVL 300
QY 301 VLLALLGVIIIAKKYFFKKEVQQL 323
DB 301 VLLALLGVIIIAKKYFFKKEVQQL 323

RESULT 14
US-10-188-012-21
; Sequence 21, Application US/10188012
; Publication No. US20030124114A1
; GENERAL INFORMATION:
; APPLICANT: McIntire, Jennifer Jones
; APPLICANT: Umetsu, Dale T.
; APPLICANT: Dekruyff, Rosemarie
; APPLICANT: Kuchroo, Vijay
; APPLICANT: Freeman, Gordon J.
; TITLE OF INVENTION: T Cell Regulatory Genes and Methods of
; FILE REFERENCE: STAN-235
; CURRENT APPLICATION NUMBER: US/10/188,012
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/302,344
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 365
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(365)
; OTHER INFORMATION: TIM-1, allele 3
US-10-188-012-21

Query Match          95.3%; Score 1666; DB 14; Length 365;
Best Local Similarity 97.9%; Pred. No. 9.4e-108;
Matches 322; Conservative 0; Mismatches 1; Indels 6; Gaps 1;

QY 1 MHPQVILSLIHLADSVAGSVKVGEGAPSVTLPCYSGAVTSMCMNRGSCSLFTCQNG 60
DB 1 MHPQVILSLIHLADSVAGSVKVGEGAPSVTLPCYSGAVTSMCMNRGSCSLFTCQNG 60
QY 61 IWWTNGTHVTKDTRYKLLGLDLSRDDVSLTIENTAVSDSGVYCCRVHRGFNDMKITV 120
DB 61 IWWTNGTHVTKDTRYKLLGLDLSRDDVSLTIENTAVSDSGVYCCRVHRGFNDMKITV 120
QY 121 SLEIVPPKVTTPPIVTTVPTVTRTSTVPTTTTTPVTTPVTTPVTTPVTTPVTTP 180
DB 121 SLEIVPPKVTTPPIVTTVPTVTRTSTVPTTTTTPVTTPVTTPVTTPVTTPVTTP 180
QY 181 TTTSVPTTTSIPTTTSVPVTTVPFVPPMPLPRQNHPEVATSPSPQPAETHPTLQGT 240
DB 181 TTTSVPTTTSIPTTTSVPVTTVPFVPPMPLPRQNHPEVATSPSPQPAETHPTLQGT 240
QY 241 IRREPTSPSYTTDNDVTVESSDGLMNNQTLFLEHSLLTANTTKGIYAGVCISVL 300
DB 241 IRREPTSPSYTTDNDVTVESSDGLMNNQTLFLEHSLLTANTTKGIYAGVCISVL 300
QY 301 VLLALLGVIIIAKKYFFKKEVQQL 323
DB 301 VLLALLGVIIIAKKYFFKKEVQQL 323

US-10-663-497-21
; Sequence 21, Application US/10663497
; Publication No. US20050095593A1
; GENERAL INFORMATION:
; APPLICANT: Dale Umetsu
; APPLICANT: Rosemarie Dekruyff
; APPLICANT: Jennifer McIntire
; APPLICANT: Gordon Freeman
; TITLE OF INVENTION: T CELL REGULATORY GENES ASSOCIATED WITH
; FILE REFERENCE: STAN-235CIP
; CURRENT APPLICATION NUMBER: US/10/663,497
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/302,344
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 10/188,012
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 365
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(365)
; OTHER INFORMATION: TIM-1, allele 3
US-10-663-497-21

Query Match          95.3%; Score 1666; DB 17; Length 365;
Best Local Similarity 97.9%; Pred. No. 9.4e-108;
Matches 322; Conservative 0; Mismatches 1; Indels 6; Gaps 1;

QY 1 MHPQVILSLIHLADSVAGSVKVGEGAPSVTLPCYSGAVTSMCMNRGSCSLFTCQNG 60
DB 1 MHPQVILSLIHLADSVAGSVKVGEGAPSVTLPCYSGAVTSMCMNRGSCSLFTCQNG 60
QY 61 IWWTNGTHVTKDTRYKLLGLDLSRDDVSLTIENTAVSDSGVYCCRVHRGFNDMKITV 120
DB 61 IWWTNGTHVTKDTRYKLLGLDLSRDDVSLTIENTAVSDSGVYCCRVHRGFNDMKITV 120
QY 121 SLEIVPPKVTTPPIVTTVPTVTRTSTVPTTTTTPVTTPVTTPVTTPVTTPVTTP 180
DB 121 SLEIVPPKVTTPPIVTTVPTVTRTSTVPTTTTTPVTTPVTTPVTTPVTTPVTTP 180
QY 181 TTTSVPTTTSIPTTTSVPVTTVPFVPPMPLPRQNHPEVATSPSPQPAETHPTLQGT 240
DB 181 TTTSVPTTTSIPTTTSVPVTTVPFVPPMPLPRQNHPEVATSPSPQPAETHPTLQGT 240
QY 241 IRREPTSPSYTTDNDVTVESSDGLMNNQTLFLEHSLLTANTTKGIYAGVCISVL 300
DB 241 IRREPTSPSYTTDNDVTVESSDGLMNNQTLFLEHSLLTANTTKGIYAGVCISVL 300
QY 301 VLLALLGVIIIAKKYFFKKEVQQL 323
DB 301 VLLALLGVIIIAKKYFFKKEVQQL 323
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Db 301 VCISVLVLLGLGVIIAKYFFKKEVQOL 329

Search completed: June 29, 2005, 09:33:01
Job time : 210.324 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 08:57:16 ; Search time 45.9332 Seconds
(without alignments)
542.805 Million cell updates/sec

Title: US-10-718-321-7

Perfect score: 1749

Sequence: 1 MHPQVILSLHLADSVAG.....FFKKEVQQLRPHKSCIHQRE 334

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/1aa/5A COMB.pep:*
- 2: /cgn2_6/prodata/1/1aa/5B COMB.pep:*
- 3: /cgn2_6/prodata/1/1aa/6A COMB.pep:*
- 4: /cgn2_6/prodata/1/1aa/6B COMB.pep:*
- 5: /cgn2_6/prodata/1/1aa/6C COMB.pep:*
- 6: /cgn2_6/prodata/1/1aa/6D COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1749	100.0	334	4	US-09-197-970B-7
2	1309	74.8	451	1	US-08-287-001A-2
3	1309	74.8	451	5	PCT-US95-09941-2
4	522.5	29.9	307	4	US-09-197-970B-3
5	292	16.7	281	1	US-08-487-748A-9
6	292	16.7	281	1	US-08-487-748A-10
7	292	16.7	281	3	US-08-480-070C-10
8	292	16.7	281	3	US-08-829-525-10
9	292	16.7	281	3	US-08-609-583A-10
10	292	16.7	281	3	US-08-937-399-10
11	292	16.7	281	4	US-09-310-367-10
12	292	16.7	281	4	US-09-032-337-10
13	292	16.7	281	4	US-09-464-231-10
14	267	15.3	301	3	US-08-829-525-24
15	267	15.3	301	3	US-08-609-583A-24
16	267	15.3	301	3	US-08-937-399-24
17	267	15.3	301	4	US-09-310-367-24
18	267	15.3	301	4	US-09-032-337-24
19	267	15.3	301	4	US-09-464-231-24
20	235	13.4	786	3	US-09-103-429A-3
21	235	13.4	805	3	US-09-103-429A-4
22	232.5	13.3	288	4	US-09-216-393B-341
23	232.5	13.3	288	4	US-09-216-393B-344
24	229	13.1	788	4	US-09-294-663-3
25	229	13.1	807	4	US-09-294-663-4
26	227.5	13.0	1721	3	US-08-700-651-5
27	227.5	13.0	1721	3	US-08-928-361B-6

28	227.5	13.0	1721	4	US-09-588-995A-6	Sequence 6, Appli
29	227.5	13.0	1837	3	US-08-928-361B-5	Sequence 5, Appli
30	227.5	13.0	1837	4	US-09-588-995A-5	Sequence 5, Appli
31	226.5	13.0	5179	4	US-09-538-092-1258	Sequence 1258, Ap
32	225	12.9	216	3	US-08-928-361B-27	Sequence 27, Appl
33	222	12.7	216	3	US-08-928-361B-8	Sequence 8, Appli
34	222	12.7	216	4	US-09-588-995A-8	Sequence 8, Appli
35	221.5	12.7	175	3	US-08-700-651-12	Sequence 12, Appl
36	221.5	12.7	175	3	US-08-928-361B-17	Sequence 17, Appl
37	221.5	12.7	175	4	US-09-588-995A-17	Sequence 17, Appl
38	219.5	12.6	150	3	US-08-928-361B-18	Sequence 18, Appl
39	219.5	12.6	150	4	US-09-588-995A-18	Sequence 18, Appl
40	219.5	12.6	249	3	US-08-700-651-15	Sequence 15, Appl
41	219.5	12.6	249	3	US-08-928-361B-20	Sequence 20, Appl
42	219.5	12.6	249	4	US-09-588-995A-20	Sequence 20, Appl
43	208.5	11.9	138	3	US-08-700-651-10	Sequence 10, Appl
44	208.5	11.9	138	3	US-08-928-361B-15	Sequence 15, Appl
45	208.5	11.9	138	4	US-09-588-995A-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1

US-09-197-970B-7
; Sequence 7, Application US/09197970B
; Patent No. 6664385
; GENERAL INFORMATION:
; APPLICANT: Michele Sanicola-Nadel
; Joseph V. Bonventre
; Catherine A. Hession
; Takaharu Ichimura
; Henry Wei
; Richard L. Cate
; TITLE OF INVENTION: MODULATORS OF TISSUE REGENERATION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/197,970B
FILING DATE: 23-No. 6664385-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/018,228
FILING DATE: 24-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Levine, Leslie M.
REGISTRATION NUMBER: 35,245
REFERENCE/DOCKET NUMBER: A010 PCT CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 679-2810
TELEFAX: (617) 679-2838
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 334 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-197-970B-7

Query Match 100.0%; Score 1749; DB 4; Length 334;
Best Local Similarity 100.0%; Pred. No. 7.9e-136;

Matches 334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHPQVILSLIHLADSVAGSVKVGEGAPSVTLPHYSGAVTSMCWNRGCSLFTCQNG 60
DB 1 MHPQVILSLIHLADSVAGSVKVGEGAPSVTLPHYSGAVTSMCWNRGCSLFTCQNG 60
QY 61 IWTNGTHVTRKDYKLLGLDLSRRDVSLLTENTAVSDSGVYCCRVHRGFNDMKITV 120
DB 61 IWTNGTHVTRKDYKLLGLDLSRRDVSLLTENTAVSDSGVYCCRVHRGFNDMKITV 120
QY 121 SLEIAPPKV-----TTTPIVTTVP 139
DB 121 SLEIAPPKV-----TTTPIVTTVP 139
QY 140 TTTTVPPTTTSIPPTTTSVPPTTTSVPPTTTSVPPTTTSVPPTTTSVPPTTTSVP 182
DB 140 TTTTVPPTTTSIPPTTTSVPPTTTSVPPTTTSVPPTTTSVPPTTTSVPPTTTSVP 182
QY 181 TTTTVPPTTTSIPPTTTSVPPTTTSVPPTTTSVPPTTTSVPPTTTSVPPTTTSVP 240
DB 181 TTTTVPPTTTSIPPTTTSVPPTTTSVPPTTTSVPPTTTSVPPTTTSVPPTTTSVP 240
QY 241 IRREPTSPPLSYTTDGDNDVTSSDGLWNNNOTOLFLEHSLLTANTTKGIYAGVCISVL 300
DB 241 IRREPTSPPLSYTTDGDNDVTSSDGLWNNNOTOLFLEHSLLTANTTKGIYAGVCISVL 300
QY 301 VLLALLGVIIIAKKYFFKKEVQQLRPHKSCIHORE 334
DB 301 VLLALLGVIIIAKKYFFKKEVQQLRPHKSCIHORE 334

RESULT 2

US-08-287-001A-2
; Sequence 2, Application US/08287001A
; Patent No. 5622861
; GENERAL INFORMATION:
; APPLICANT: KAPLAN, GERARDO
; APPLICANT: FEINSTONE, STEPHEN M.
; TITLE OF INVENTION: HEPATITIS A VIRUS RECEPTOR AND METHODS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, The Candler Bldg, 127 Peachtree
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Spratt, Gwedolyn D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 1414.621
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-287-001A-2

Query Match 74.8%; Score 1309; DB 1; Length 451;
Best Local Similarity 63.3%; Pred. No. 1.6e-99;
Matches 255; Conservative 36; Mismatches 32; Indels 80; Gaps 3;

QY 1 MHPQVILSLIHLADSVAGSVKVGEGAPSVTLPHYSGAVTSMCWNRGCSLFTCQNG 60
DB 1 MHPQVILSLIHLADSVAGSVKVGEGAPSVTLPHYSGAVTSMCWNRGCSLFTCQNG 60
QY 61 IWTNGTHVTRKDYKLLGLDLSRRDVSLLTENTAVSDSGVYCCRVHRGFNDMKITV 120
DB 61 IWTNGTHVTRKDYKLLGLDLSRRDVSLLTENTAVSDSGVYCCRVHRGFNDMKITV 120
QY 121 SLEIAPPKV-----TTTPIVTTVP 139
DB 121 SLEIAPPKV-----TTTPIVTTVP 139
QY 140 TTTTVPPTTTSIPPTTTSVPPTTTSVPPTTTSVPPTTTSVPPTTTSVPPTTTSVP 182
DB 140 TTTTVPPTTTSIPPTTTSVPPTTTSVPPTTTSVPPTTTSVPPTTTSVPPTTTSVP 182
QY 181 TTTTVPPTTTSIPPTTTSVPPTTTSVPPTTTSVPPTTTSVPPTTTSVPPTTTSVP 240
DB 181 TTTTVPPTTTSIPPTTTSVPPTTTSVPPTTTSVPPTTTSVPPTTTSVPPTTTSVP 240
QY 183 T-----SVPTTTSIPPTTTSVPPTTTSVPPTTTSVPPTTTSVPPTTTSVP 220
DB 183 T-----SVPTTTSIPPTTTSVPPTTTSVPPTTTSVPPTTTSVPPTTTSVP 220
QY 241 TTTTVPPTTTSIPPTTTSVPPTTTSVPPTTTSVPPTTTSVPPTTTSVPPTTTSVP 300
DB 241 TTTTVPPTTTSIPPTTTSVPPTTTSVPPTTTSVPPTTTSVPPTTTSVPPTTTSVP 300
QY 221 ATSPSSPOPAETHPTTLOGAIREPTSSPLSYTTDGDNDVTSSDGLWNNNOTOLFLEH 280
DB 301 ATSPSSPOPAETHPTTLOGAIREPTSSPLSYTTDGDNDVTSSDGLWNNNOTOLFLEH 360
QY 281 SLLTANTTKGIYAGVCISVLVLLALLGVIIIAKKYFFKKEVQQL 323
DB 361 SPQWNTTEGIYAGVCISVLVLLALLGVIIIAKKYFFKKEVQQL 403

RESULT 3

PCT-US95-09941-2
; Sequence 2, Application PC/TUS9509941
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HEPATITIS A VIRUS RECEPTOR AND METHODS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, The Candler Bldg, 127 Peachtree
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/287,001
; FILING DATE: 5 AUG 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Spratt, Gwedolyn D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 1414.621
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-09941-2

Query Match 74.8%; Score 1309; DB 5; Length 451;

Best Local Similarity 63.3%; Pred. No. 1.6e-99;
Matches 255; Conservative 36; Mismatches 32; Indels 80; Gaps 3;
QY 1 MHPQVILSLIHLADSVAGSVKVGEGAPSVTLPCYSGAVTSMCMNRGSCSLFTCONG 60
DB 1 MHLQVILSLIHLADSVADSVNVDGAGLSITLPCRYNGAITSMCNNGTSCVSCPDG 60
QY 61 IWTNGTHVTRKQTRYKLLGDLRRDVSLLTAVSDSGVYCCRVHRGWFNDKMTIV 120
DB 61 IWTNGTHVTRKQTRYKLLGDLRRDVSLLTAVSDSGVYCCRVHRGWFNDKMTIV 120
QY 121 SLEIVPPKV-----TTTTPIVTVTP 139
DB 121 SLEIVPPKV-----TTTTPIVTVTP 139
QY 140 TTTTPTTTPPTTTTTP-----TTTTPTTMSIPTTTTPTTMTVST 182
DB 181 TTTTPTTTPPTTTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTP 180
QY 183 T-----SVPTTMSIPTTTSVPVTTTSTVTFVPPMPLPRQNHBPV 220
DB 241 TTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTP 300
QY 221 ATSPSSPOPAETHPTTLOGAIRREPTSSPLSYTTDGNVTSTSSDGLWNNOTOLPLEH 280
DB 301 ATSPSSPOPAETHPTTLOGAIRREPTSSPLSYTTDGNVTSTSSDGLWNNOTOLPLEH 280
QY 281 SLLTANTKGIYAGVCSIVLVLLALGVIIIAKKYFPKKEVQQL 323
DB 361 SPQWNTTEGIYAGVCSIVLVLLALGVIIIAKKYFPKKEIQL 403

RESULT 4
US-09-197-970B-3
; Sequence 3, Application US/09197970B
; Patent No. 6664385
; GENERAL INFORMATION:
; APPLICANT: Michele Sanicola-Nadel
; Joseph V. Bonventre
; Catherine A. Hession
; Takaharu Ichimura
; Henry Wei
; Richard L. Cate
; TITLE OF INVENTION: MODULATORS OF TISSUE REGENERATION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/197,970B
; FILING DATE: 23-NOV-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/018,228
; FILING DATE: 24-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Levine, Leslie M.
; REGISTRATION NUMBER: 35,245
; REFERENCE/DOCKET NUMBER: A010 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 679-2810
; TELEFAX: (617) 679-2838
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid

LENGTH: 307 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-197-970B-3
Query Match 29.9%; Score 522.5; DB 4; Length 307;
Best Local Similarity 39.4%; Pred. No. 4.2e-35;
Matches 128; Conservative 39; Mismatches 93; Indels 65; Gaps 12;
QY 4 QVILSLIHLADSVAGSVKVGEGAPSVTLPCYSGAVTSMCMNRGSCSLFTCONG 61
DB 5 QVILSLIHLADSVAGSVKVGEGAPSVTLPCYSGAVTSMCMNRGSCSLFTCONG 64
QY 62 VWTNGTHVTRKQTRYKLLGDLRRDVSLLTAVSDSGVYCCRVHRGWFNDKMTIVS 121
DB 65 IWTNGQVYTRSSGRYNIKRISEGDVSLTIENSVDSDGLYCCRVHRGWFNDKMTIVS 124
QY 122 LEIVPPKVTTPIVTVTVTTTSTVSTVPT-----TTTTPTTPTTPTTPTTPTTPTTPTT 179
DB 125 LE-VKPEIPTSP-----PTRPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 153
QY 180 STTTSVPPTTSTPTTSTVPTTSTVPTTSTVPTTSTVPTTSTVPTTSTVPTTSTVPTT 239
DB 154 TRSTHPTTSTVSTST-----PTPEQTQTHKPEITT-----FYAHETT----- 191
QY 240 AIRREPTSSPLSYTTDGNVTSTSSDGLWNNOTOLPLEHSLLTANTKGIYAGVCSIV 299
DB 192 ---AEVTETPSVT-PADWNGT-VT-SSEAWNNHTVRIPLRKP--QRNPTKGFVGVMSVAA 244
QY 300 LVLLALGVIIIAKKY-FPKKEVQQL 323
DB 245 LVLLALGVIIIAKKY-FPKKEVQQL 269
RESULT 5
US-08-487-748A-9
; Sequence 9, Application US/08487748A
; Patent No. 5721351
; GENERAL INFORMATION:
; APPLICANT: Levinson, Douglas A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,748A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid

TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-487-748A-9

Query Match 16.7%; Score 292; DB 1; Length 281;
Best Local Similarity 27.5%; Pred. No. 3.2e-16;
Matches 89; Conservative 37; Mismatches 78; Indels 120; Gaps 8;

QY 6 VILSLILHLADSVAGSVKVGGEAGPSVTLPCY-----SGAVTSMCWNRGSCSLFTQNGI 61
DB 10 VLLQLLARSLELDGYK--EVGNAYLPCSYTLPTSGLVPMCWGKGFPCWISQCTNEL 67
QY 62 VWTNGTHVYKOTRYKLLGDLRRDVSLLTENTAVSDSGVYCCRVHRGFNMDKITS 121
DB 68 LRTDERNVYKSSRYQLKGLNKGDSLIKNVTLDDHGYCCRIQFPLMNDKLELK 127
QY 122 LEIVPPKVTTPPIVTTVPTVTTVTSITVPTTTTPTVTTTPTVTTTPTVTTTPTVTTT 181
DB 128 LDIAKAVT----- 136
QY 182 TTSVPTTTSIPTTSVPVTTTSTVTFVPPMPLPRQNHPEVATSPSPQPAETHPTTLOGAI 241
DB 137 -----PAQTAHGDSTTAS-----PRTL----- 153
QY 242 RREPTSSPLSYTTDGDNDVTTESSDGLWNNNOTOLF-----LEHSLLTANTTKGIYAGVC 296
DB 154 -----TTERNGSETQTLVTLHNNNGTKISTWADEIKDSGETIRT--AIHIGVG 199
QY 297 ISV-LVLLALLGVIIAKYFPKKE 319
DB 200 VSAGLTALIIIGVILKWKYCKKK 223

RESULT 6
US-08-487-748A-10
; Sequence 10, Application US/08487748A
; Patent No. 5721351
; GENERAL INFORMATION:
; APPLICANT: Levinson, Douglas A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,748A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-487-748A-10

Query Match 16.7%; Score 292; DB 1; Length 281;
Best Local Similarity 27.5%; Pred. No. 3.2e-16;
Matches 89; Conservative 37; Mismatches 78; Indels 120; Gaps 8;

QY 6 VILSLILHLADSVAGSVKVGGEAGPSVTLPCY-----SGAVTSMCWNRGSCSLFTQNGI 61
DB 10 VLLQLLARSLELDGYK--EVGNAYLPCSYTLPTSGLVPMCWGKGFPCWISQCTNEL 67
QY 62 VWTNGTHVYKOTRYKLLGDLRRDVSLLTENTAVSDSGVYCCRVHRGFNMDKITS 121
DB 68 LRTDERNVYKSSRYQLKGLNKGDSLIKNVTLDDHGYCCRIQFPLMNDKLELK 127
QY 122 LEIVPPKVTTPPIVTTVPTVTTVTSITVPTTTTPTVTTTPTVTTTPTVTTTPTVTTT 181
DB 128 LDIAKAVT----- 136
QY 182 TTSVPTTTSIPTTSVPVTTTSTVTFVPPMPLPRQNHPEVATSPSPQPAETHPTTLOGAI 241
DB 137 -----PAQTAHGDSTTAS-----PRTL----- 153
QY 242 RREPTSSPLSYTTDGDNDVTTESSDGLWNNNOTOLF-----LEHSLLTANTTKGIYAGVC 296
DB 154 -----TTERNGSETQTLVTLHNNNGTKISTWADEIKDSGETIRT--AIHIGVG 199
QY 297 ISV-LVLLALLGVIIAKYFPKKE 319
DB 200 VSAGLTALIIIGVILKWKYCKKK 223

RESULT 7
US-08-480-070C-10
; Sequence 10, Application US/08480070C
; Patent No. 6066498
; GENERAL INFORMATION:
; APPLICANT: Levinson, Douglas A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,070C
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-480-070C-10

Query Match 16.7%; Score 292; DB 3; Length 281;
Best Local Similarity 27.5%; Pred. No. 3.2e-16;

Matches 89; Conservative 37; Mismatches 78; Indels 120; Gaps 8;

QY 6 VILSLILHLADSVAGSKVGEAGPSVTLPCY-----SGAVTSMCNRGSCSLFTQNGI 61
DB 10 VLLLLQLLLARSLEDEGKVV--EVGNAYLPCS YTLPTSGTLVPMCKGKGFPCWQSQTNEL 67
QY 62 VWTNGTHVTRKDRYKLGDLRRDVS LTIENAVSDSGVYCCRVHRGWFNMDKITVS 121
DB 68 LRTDERNVYQKSSRYQLKGLNKGDSVLI IKNVTLDDHGTGCCRIQFPGLMNDKKLELK 127
QY 122 LEIVPPKVTTPITVTTVPTVTTVTSTTTPVTTTTPVTTTTPVTTTTPVTTTTPVTTT 181
DB 128 LDIKAQVT-----PRTL----- 136
QY 182 TTSVPTTTSIPTTSVPVTTTSTFVPPMPLPRQNHVPATSPSPQPAETHPTTTLQGA 241
DB 137 -----PAQTAHGDSTTAS-----PRTL----- 153
QY 242 RREPTSSPLYSTTGDNDVTSSDGLWNNQTLF-----LEHSLLTANTTKGIYAGVC 296
DB 154 -----TTERNGSETQTLVTLHNNNGTKISTWADEIKDSGETIRT--AIHIGVG 199
QY 297 ISV-LVLLALLGVIIAKYFFKKE 319
DB 200 VSAGLTLALIIGVLILKWKYSCKKK 223

RESULT 8

US-08-829-525-10
; Sequence 10, Application US/08829525
; Patent No. 6084083
; GENERAL INFORMATION:
; APPLICANT: Levinson, Douglas A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,525
; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/609,583
; FILING DATE: 01-MAR-1996
; APPLICATION NUMBER: US 08/487,748
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/398,633
; FILING DATE: 03-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-081
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein

US-08-829-525-10

Query Match 16.7%; Score 292; DB 3; Length 281;
Best Local Similarity 27.5%; Pred. No. 3.2e-16;
Matches 89; Conservative 37; Mismatches 78; Indels 120; Gaps 8;

QY 6 VILSLILHLADSVAGSKVGEAGPSVTLPCY-----SGAVTSMCNRGSCSLFTQNGI 61
DB 10 VLLLLQLLLARSLEDEGKVV--EVGNAYLPCS YTLPTSGTLVPMCKGKGFPCWQSQTNEL 67
QY 62 VWTNGTHVTRKDRYKLGDLRRDVS LTIENAVSDSGVYCCRVHRGWFNMDKITVS 121
DB 68 LRTDERNVYQKSSRYQLKGLNKGDSVLI IKNVTLDDHGTGCCRIQFPGLMNDKKLELK 127
QY 122 LEIVPPKVTTPITVTTVPTVTTVTSTTTPVTTTTPVTTTTPVTTTTPVTTTTPVTTT 181
DB 128 LDIKAQVT-----PRTL----- 136
QY 182 TTSVPTTTSIPTTSVPVTTTSTFVPPMPLPRQNHVPATSPSPQPAETHPTTTLQGA 241
DB 137 -----PAQTAHGDSTTAS-----PRTL----- 153
QY 242 RREPTSSPLYSTTGDNDVTSSDGLWNNQTLF-----LEHSLLTANTTKGIYAGVC 296
DB 154 -----TTERNGSETQTLVTLHNNNGTKISTWADEIKDSGETIRT--AIHIGVG 199
QY 297 ISV-LVLLALLGVIIAKYFFKKE 319
DB 200 VSAGLTLALIIGVLILKWKYSCKKK 223

RESULT 9

US-08-609-583A-10
; Sequence 10, Application US/08609583A
; Patent No. 6204371
; GENERAL INFORMATION:
; APPLICANT: Levinson, Douglas A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,583A
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,748
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/398,633
; FILING DATE: 03-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-048
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid

```
;
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-609-583A-10

Query Match      16.7%; Score 292; DB 3; Length 281;
Best Local Similarity 27.5%; Pred. No. 3.2e-16;
Matches 89; Conservative 37; Mismatches 78; Indels 120; Gaps 8;

QY 6 VILSLILHLASVAGSVKVGEGAGPSVTLPCY-----SGAVTSMCWNRGSCSLFTCQNGI 61
Db 10 VLLQLQLLARSLEDEYKV--EVGNAYLPCSYLPTSGTLVPMCWGKGFCEWFSQCTNEL 67
QY 62 VWTNGTHVYRKDTRYKLLGDLRRDVSLLTENTAVSDGVCYCCVHRHGFNFMKMTVS 121
Db 68 LRTDERNVYQKSSRYQLKGLNKGDSLLIKNVLDHGYCCRIQPPGLMNDKKLELK 127
QY 122 LEIVPPKVTTPITVTVPTVTRTSTVPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 181
Db 128 LDIAKAAVT----- 136
QY 182 TTSVPTTTSIPTTSVPVTVTVTFVPPMPLPRQNHPEVATSPSPQPAETHPTTLOGAI 241
Db 137 -----PAQTAHGDSTTAS-----PRTL----- 153
QY 242 RREPTSSPLYSTTDCGNDVTVESSDGLMNNNOTOLF-----LEHSLLTANTTKGIYAGVC 296
Db 154 -----TTERNGSETQTLVTLNHNNGTKISTWADEIKDSGETIRT--AIHIGVG 199

RESULT 10
US-08-937-399-10
; Sequence 10, Application US/08937399
; Patent No. 6288218
; GENERAL INFORMATION:
; APPLICANT: Levinson, Douglas A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITL OF INVENTION: TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,399
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,583
; FILING DATE: 01-MAR-1996
; APPLICATION NUMBER: US 08/487,748
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/398,633
; FILING DATE: 03-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-048
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE

;
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-937-399-10

Query Match      16.7%; Score 292; DB 3; Length 281;
Best Local Similarity 27.5%; Pred. No. 3.2e-16;
Matches 89; Conservative 37; Mismatches 78; Indels 120; Gaps 8;

QY 6 VILSLILHLASVAGSVKVGEGAGPSVTLPCY-----SGAVTSMCWNRGSCSLFTCQNGI 61
Db 10 VLLQLQLLARSLEDEYKV--EVGNAYLPCSYLPTSGTLVPMCWGKGFCEWFSQCTNEL 67
QY 62 VWTNGTHVYRKDTRYKLLGDLRRDVSLLTENTAVSDGVCYCCVHRHGFNFMKMTVS 121
Db 68 LRTDERNVYQKSSRYQLKGLNKGDSLLIKNVLDHGYCCRIQPPGLMNDKKLELK 127
QY 122 LEIVPPKVTTPITVTVPTVTRTSTVPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 181
Db 128 LDIAKAAVT----- 136
QY 182 TTSVPTTTSIPTTSVPVTVTVTFVPPMPLPRQNHPEVATSPSPQPAETHPTTLOGAI 241
Db 137 -----PAQTAHGDSTTAS-----PRTL----- 153
QY 242 RREPTSSPLYSTTDCGNDVTVESSDGLMNNNOTOLF-----LEHSLLTANTTKGIYAGVC 296
Db 154 -----TTERNGSETQTLVTLNHNNGTKISTWADEIKDSGETIRT--AIHIGVG 199

RESULT 11
US-09-310-367-10
; Sequence 10, Application US/09310367
; Patent No. 6414117
; GENERAL INFORMATION:
; APPLICANT: Levinson, Douglas A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITL OF INVENTION: TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/310,367
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,525
; FILING DATE: 28-MAR-1997
; APPLICATION NUMBER: US 08/609,583
; FILING DATE: 01-MAR-1996
; APPLICATION NUMBER: US 08/487,748
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/398,633
; FILING DATE: 03-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
```

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;
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-081
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-310-367-10

Query Match      16.7%; Score 292; DB 4; Length 281;
Best Local Similarity 27.5%; Pred. No. 3.2e-16;
Matches 89; Conservative 37; Mismatches 78; Indels 120; Gaps 8;

QY 6 VLSLILHLADSVAGSVKVGGEAGPSVTLPCHY-----SGAVTSMCWNRGSCSLFTQNGI 61
Db 10 VLLLLQLLARSLEDEGYK--EVGNAYLPCSYTLPTSGTLVPMCMGKFCFWSQCTNEL 67
QY 62 VMTNGTHYTRKDYKLLGLDLSRRDVSILTIENTAVSDSGVYCCRVHRGWENDMKITVS 121
Db 68 LRTDERNTYQSSRYQLKGLDNGDVSLLIKNVLDHGTCCRIQPPGLMNDKKLELK 127
QY 122 LEIVPEKVTTPITVTTVPTVTTVTRTSTTPTTTTPTTPTTPTTPTTPTTPTTPTTPTT 181
Db 128 LDIAKAVT----- 136
QY 182 TTSVPTTTSIPPTTSVPVTTTSTVTPVPMPLPRQNHPEVATSPSPQPAETHPTTLOGAI 241
Db 137 -----PAQTAHGDSTTAS-----PRTL----- 153
QY 242 RREPTSSPLYSTTGDNDTVTSSDGLWNNNOTLP-----LEHSLLTANTTKGIYAGVC 296
Db 154 -----TTERNGSETQTLVTLNHNNGTKISTWADEIKDSGETIRT--AIHIGVG 199
QY 297 ISV-LVLLALLGVIIAKKYFFKKE 319
Db 200 VSAGLTALIIIGVLLIKWYSCKK 223

RESULT 12
US-09-337-10
; Sequence 10, Application US/09032337
; Patent No. 6455685
; GENERAL INFORMATION:
; APPLICANT: Levinson, Douglas A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032.337
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/609,583
; FILING DATE: 01-MAR-1996
; APPLICATION NUMBER: US 08/487,748
; FILING DATE: 07-JUN-1995

;
; APPLICATION NUMBER: US 08/398,633
; FILING DATE: 03-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-032-337-10

Query Match      16.7%; Score 292; DB 4; Length 281;
Best Local Similarity 27.5%; Pred. No. 3.2e-16;
Matches 89; Conservative 37; Mismatches 78; Indels 120; Gaps 8;

QY 6 VLSLILHLADSVAGSVKVGGEAGPSVTLPCHY-----SGAVTSMCWNRGSCSLFTQNGI 61
Db 10 VLLLLQLLARSLEDEGYK--EVGNAYLPCSYTLPTSGTLVPMCMGKFCFWSQCTNEL 67
QY 62 VMTNGTHYTRKDYKLLGLDLSRRDVSILTIENTAVSDSGVYCCRVHRGWENDMKITVS 121
Db 68 LRTDERNTYQSSRYQLKGLDNGDVSLLIKNVLDHGTCCRIQPPGLMNDKKLELK 127
QY 122 LEIVPEKVTTPITVTTVPTVTTVTRTSTTPTTTTPTTPTTPTTPTTPTTPTTPTTPTT 181
Db 128 LDIAKAVT----- 136
QY 182 TTSVPTTTSIPPTTSVPVTTTSTVTPVPMPLPRQNHPEVATSPSPQPAETHPTTLOGAI 241
Db 137 -----PAQTAHGDSTTAS-----PRTL----- 153
QY 242 RREPTSSPLYSTTGDNDTVTSSDGLWNNNOTLP-----LEHSLLTANTTKGIYAGVC 296
Db 154 -----TTERNGSETQTLVTLNHNNGTKISTWADEIKDSGETIRT--AIHIGVG 199
QY 297 ISV-LVLLALLGVIIAKKYFFKKE 319
Db 200 VSAGLTALIIIGVLLIKWYSCKK 223

RESULT 13
US-09-464-231-10
; Sequence 10, Application US/09464231
; Patent No. 6562343
; GENERAL INFORMATION:
; APPLICANT: Levinson, Douglas A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/464,231
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US/08/609,583
; FILING DATE: 01-MAR-1996
; APPLICATION NUMBER: US 08/487,748
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/398,633
; FILING DATE: 03-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-048
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-464-231-10

Query Match      16.7%; Score 292; DB 4; Length 281;
Best Local Similarity 27.5%; Pred. No. 3.2e-16;
Matches 89; Conservative 37; Mismatches 78; Indels 120; Gaps 8;

QY 6 VILSLILHLADSVAGSKVGEAGPSVTLPCHY-----SGAVTSMCWNRGSCSLFTCQNGI 61
DB 10 VILLQLLLARSLEGGYK--EVGNAYLPCSYTLFTSGTLVPMCWGKGFCFWSQCTNEL 67
QY 62 VWTNGTHVYRKDTRYKLLGDLRRDVSLLTIENTAVSDSGVYCCRVHRGNFNDMKITVS 121
DB 68 LRTDERNVYKSSRYQLKDLNGDVSLLIKNVLDHGYCCRIQFPGLMNDKLELK 127
QY 122 LEIVPPKVTTPPIVTVPTVTRTSTVPTTTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 181
DB 128 LDIKAAKVT-----PAQTAHGSSTAS-----PRTL----- 153
QY 182 TTSVPTTTSIPTTISVPVTTTSTVPVPMPLPRQNHEPVATSPSPQPAETHPTTLOGAI 241
DB 137 -----PAQTAHGSSTAS-----PRTL----- 153
QY 242 RREPTSSPLYSTTDGNTVTTESSDGLMNNNOTQLF-----LEHSLLTANTTKGIYAGVC 296
DB 154 -----TTERNGSETQLTLVLENNNGTKISTWADEIKDSGETIRT--ALHIGVG 199
QY 297 ISV-LVLLALLGVIIAKYFFKKE 319
DB 200 VSAGLTALIIIGVLILKWYSCKK 223

RESULT 14
US-08-829-525-24
; Sequence 24, Application US/08829525
; Patent No. 6084083
; GENERAL INFORMATION:
; APPLICANT: Levinson, Douglas A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/829,525
; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/609,583
; FILING DATE: 01-MAR-1996
; APPLICATION NUMBER: US 08/487,748
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/398,633
; FILING DATE: 03-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-081
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-829-525-24

Query Match      15.3%; Score 267; DB 3; Length 301;
Best Local Similarity 26.9%; Pred. No. 4e-14;
Matches 88; Conservative 32; Mismatches 99; Indels 108; Gaps 11;

QY 6 VILSLILHLADSVAGSKVGEAGPSVTLPCHY-----GAVTSMCWNRGSCSLFTCQNGI 61
DB 10 VILLLELLLTSTR--SEVEYRAEVGNAYLPCFYTPAAPGNLVPVCGWKGACPVFCGNV 67
QY 62 VWTNGTHVYRKDTRYKLLGDLRRDVSLLTIENTAVSDSGVYCCRVHRGNFNDMKITVS 121
DB 68 LRTDERDNYV-WTSRYWLANGDFRKGDVSLTIENVTLADSGIYCCRIQIPGIMNDEKFNK 126
QY 122 LEIVPPKVTTPPIVTVPTVTRTSTVPTTTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 181
DB 127 LVIPKAKVTPAP-----TLQRDFTAAFPRLMTT-- 154
QY 182 TTSVPTTTSIPTTISVPVTTTSTVFPVPMPLPRQNHEPVATSP--SSQPAETHPTTLOG 239
DB 155 -----RHGHPAEQTQLGSLPDINLTQISTLAN 181
QY 240 AIRREPTSSPLYSTTDGNTVTTESSDGLMNNNOTQLFLEHSLLTANTTKGIY--AGVCI 297
DB 182 ELR-----DSRLANDLRDSGATI-----RIGIYIGAGICA 211
QY 298 SVLVLLALLGVIIAKYFFKKE-VQQL 323
DB 212 G-LALALIFGALIFKWIYSHSKEKIQNL 237

RESULT 15
US-08-609-583A-24
; Sequence 24, Application US/08609583A
; Patent No. 6204371
; GENERAL INFORMATION:
; APPLICANT: Levinson, Douglas A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
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Search completed: June 29, 2005, 09:02:59
Job time : 47.9332 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 08:57:16 ; Search time 237.54 Seconds
(without alignments)
543.815 Million cell updates/sec

Title: US-10-718-321-7
Perfect score: 1749
Sequence: 1 MHPQVILSLHLADSVAG.....FFKKEVQQLRPHKSHQRE 334

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1749	100.0	334	2	AAW38336 Human kid
2	1749	100.0	334	6	AAO26679 KIM-1 rel
3	1749	100.0	334	8	ADQ76696 Human kid
4	1694	96.3	359	6	ABR58592 Human can
5	1684	96.3	359	6	ABP70438 Amino aci
6	1684	96.3	359	6	ABR48174 Human bia
7	1684	96.3	359	6	AAO26680 KIM-1 rel
8	1684	96.3	359	7	ADE36594 Human NOV
9	1694	96.3	359	7	ADN38994 Cancer/an
10	1694	96.3	359	8	ADQ76690 Human kid
11	1679	96.0	359	6	ABP70439 Amino aci
12	1671	95.5	359	6	ABP70441 Amino aci
13	1666	95.3	365	6	ABP70440 Amino aci
14	1655.5	94.7	364	6	ABP70442 Amino aci
15	1643.5	94.0	364	6	ABP70443 Amino aci
16	1587	90.7	339	7	ADN36618 Plasmid p
17	1587	90.7	339	7	ADN36618 Human NOV
18	1529	87.4	298	8	ADQ76693 Human KIM
19	1529	87.4	518	8	ADQ76691 Human KIM
20	1393	79.6	263	7	ADN36629 Human NOV
21	1393	79.6	263	7	ADN36622 Plasmid p
22	1393	79.6	263	7	ADN366596 Human NOV
23	1306	74.7	451	2	AAK92803 Hepatitis
24	707	40.4	357	8	ADQ76692 Human KIM
25	592	33.8	108	7	ADN36598 Human NOV

ALIGNMENTS

RESULT 1
AAW38336
ID AAW38336 standard; protein; 334 AA.
XX
AC AAW38336;
XX
DT 21-MAY-1998 (first entry)
XX
DE Human kidney injury related molecule (KIM).
XX
KW Kidney injury related molecule; KIM; human; renal disease; injury;
KW nephritis; tissue regeneration; therapy; monoclonal antibody.
XX
OS Homo sapiens.
XX
PN WO9744460-A1.
XX
PD 27-NOV-1997.
XX
PF 23-MAY-1997; 97WO-US009303.
XX
PR 24-MAY-1996; 96US-0018229P.
PR 23-AUG-1996; 96US-0023442P.
(BIOJ) BIOGEN INC.
Sanicola-Nadel M, Bonventre JV, Hession CA, Ichimura T, Wei H;
Cate RL;
WPI; 1998-018514/02.
DNA encoding kidney injury related molecule - which is upregulated in injured or regenerating tissue, useful to promote growth of new tissue and survival of damaged tissue.
Claim 9; Page 46-47; 68pp; English.
This protein, designated kidney injury related molecule (KIM), is up-regulated in injured or regenerating tissue. Its amino acid sequence was deduced from a clone (see AAR96035) obtained from a human embryonic liver library. A 572-amino acid (see AAW38335) and a 307-amino acid rat KIM (see AAW38334) are also claimed. Recombinant KIM polypeptides can be expressed in prokaryotic and eukaryotic host cells using a claimed process. Soluble variants fused to a toxin, imageable compound or radionuclide, and IGG fusion proteins are also claimed. KIM, or an agonist, can be used to treat renal disease and to promote the growth of new tissue or the survival of damaged tissue, generally in conditions where the binding of specific ligand to KIM stimulates cell growth, maintains

26	522.5	29.9	307	2	AAW38334	AAW38334 Rat kidne
27	519	29.7	305	6	ABP70430	Abp70430 Amino aci
28	491.5	28.1	282	6	ABP70431	Abp70431 Amino aci
29	458	26.2	465	8	ADQ76695	Adq76695 Mouse kim
30	432	24.7	81	6	AAO26678	Aao26678 Human KIM
31	405	23.2	345	6	ABP70436	Abp70436 Amino aci
32	401	22.9	305	6	ABP70432	Abp70432 Amino aci
33	401	22.9	305	6	ABP70433	Abp70433 Amino aci
34	401	22.9	345	6	ABP70437	Abp70437 Amino aci
35	367.5	21.0	378	4	AAW39027	Aaw39027 Human pol
36	367.5	21.0	378	6	ABP70446	Abp70446 Amino aci
37	367.5	21.0	379	2	AAW25768	Aay25768 Human sec
38	366.5	21.0	378	6	ABP70447	Abp70447 Amino aci
39	321	18.4	183	2	AAW38395	Aay38395 Human sec
40	292	16.7	281	2	AAW01047	Aaw01047 Product o
41	292	16.7	281	3	AAW97056	Aay97056 Murine T
42	292	16.7	281	4	AAW50696	Aab50696 Mouse 200
43	292	16.7	281	4	AAW59162	Aab59162 Murine 20
44	292	16.7	281	4	AAW50225	Aab50225 Mouse 200
45	292	16.7	281	4	AAW81511	Aab81511 Murine TH

CC cellular differentiation or reduces apoptosis, e.g. in cases of renal
CC failure, nephritis, kidney transplants, toxic or hypoxic injury. A
CC monoclonal antibody specific for KIM can be used to treat renal disease,
CC e.g. where binding of KIM to ligand results in neoplasia, loss of
CC cellular function, susceptibility to apoptosis or promotion of
CC inflammation, deliver imaging agents to KIM expressing cells in vivo or
CC in vitro and measure KIM concentration by immunoassay.
CC Damage/regeneration of renal cells can be determined by measuring KIM,
CC particularly to diagnose or monitor the progress of disease or therapy.
CC KIM-expressing tumour cells can be inhibited by treatment with a fusion
CC protein comprising KIM ligand or Mab with a toxin or radionuclide, and
CC tumour cells that express KIM ligand can be inhibited with similarly
CC tagged KIM or anti-KIM ligand antibody
XX
SQ Sequence 334 AA;

Query Match 100.0%; Score 1749; DB 2; Length 334;
Best Local Similarity 100.0%; Pred. No. 7.1e-118;
Matches 334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHPQVILSLIHLADSVAGSVKVGEGAPSVTLPCYSGAVTSCWNRGSCSLFTCQNG 60
DB |||||||
1 MHPQVILSLIHLADSVAGSVKVGEGAPSVTLPCYSGAVTSCWNRGSCSLFTCQNG 60
QY 61 IVWTNGTHVTRKDRYKLLGLDLSRRDVSLLTIENTAVSDSGVYCCRVHRGFNDMKITV 120
DB |||||||
61 IVWTNGTHVTRKDRYKLLGLDLSRRDVSLLTIENTAVSDSGVYCCRVHRGFNDMKITV 120
QY 121 SLEIVPPKVTTPITVTTPVTVTSTVPTTTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 180
DB |||||||
121 SLEIVPPKVTTPITVTTPVTVTSTVPTTTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 180
QY 181 TTSVPTTSTPTTSPVPTTTSFVPPMPLPRQNHPEVATSPSPQPAETHPTTLOGA 240
DB |||||||
181 TTSVPTTSTPTTSPVPTTTSFVPPMPLPRQNHPEVATSPSPQPAETHPTTLOGA 240
QY 241 IRREPTSSPLSYTTDGNDDVTESDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 300
DB |||||||
241 IRREPTSSPLSYTTDGNDDVTESDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 300
QY 301 VLLALLGVIIIAKKYFFKKEVQQLRPHKSCIHQRE 334
DB |||||||
301 VLLALLGVIIIAKKYFFKKEVQQLRPHKSCIHQRE 334

RESULT 2
AAO26679
ID AAO26679 standard; protein; 334 AA.

XX AAO26679;
XX 20-MAR-2003 (first entry)
XX KIM-1 related protein, SEQ ID No 7.
XX Cytostatic; gene therapy; antibody; antigen; antigen-binding;
KW proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;
KW renal disease; injury; renal cancer; human.

XX Homo sapiens.
XX WO200298920-A1.
XX 12-DEC-2002.
XX 31-MAY-2002; 2002WO-US017402.
XX 01-JUN-2001; 2001US-0295449P.
XX 04-JUN-2001; 2001US-0295907P.
XX (BIOJ) BIOGEN INC.
PA (GEO) GEN HOSPITAL CORP.

PI Bailly V, Bonventre J;
XX WPI; 2003-156845/15.
DR New antibody, antibody derivative or antigen-binding polypeptide that
PT inhibits proteolytic release of a soluble kidney injury molecule-1
PT polypeptide, useful for treating or preventing renal disease or injury,
PT e.g. renal cancer.
XX Disclosure; Page 39-40; 42pp; English.
XX The invention relates to a novel antibody, antibody derivative or antigen
CC -binding polypeptide that inhibits proteolytic release of a soluble
CC kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.
CC The antibody, antibody derivative or antigen-binding polypeptide is
CC useful for treating or preventing renal disease or injury, e.g. renal
CC cancer. The antibody is also useful for inhibiting shedding of the KIM-1
CC polypeptide. This sequence represents a protein relating to the KIM-1
CC protein of the invention
XX
SQ Sequence 334 AA;

Query Match 100.0%; Score 1749; DB 6; Length 334;
Best Local Similarity 100.0%; Pred. No. 7.1e-118;
Matches 334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHPQVILSLIHLADSVAGSVKVGEGAPSVTLPCYSGAVTSCWNRGSCSLFTCQNG 60
DB |||||||
1 MHPQVILSLIHLADSVAGSVKVGEGAPSVTLPCYSGAVTSCWNRGSCSLFTCQNG 60
QY 61 IVWTNGTHVTRKDRYKLLGLDLSRRDVSLLTIENTAVSDSGVYCCRVHRGFNDMKITV 120
DB |||||||
61 IVWTNGTHVTRKDRYKLLGLDLSRRDVSLLTIENTAVSDSGVYCCRVHRGFNDMKITV 120
QY 121 SLEIVPPKVTTPITVTTPVTVTSTVPTTTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 180
DB |||||||
121 SLEIVPPKVTTPITVTTPVTVTSTVPTTTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 180
QY 181 TTSVPTTSTPTTSPVPTTTSFVPPMPLPRQNHPEVATSPSPQPAETHPTTLOGA 240
DB |||||||
181 TTSVPTTSTPTTSPVPTTTSFVPPMPLPRQNHPEVATSPSPQPAETHPTTLOGA 240
QY 241 IRREPTSSPLSYTTDGNDDVTESDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 300
DB |||||||
241 IRREPTSSPLSYTTDGNDDVTESDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 300
QY 301 VLLALLGVIIIAKKYFFKKEVQQLRPHKSCIHQRE 334
DB |||||||
301 VLLALLGVIIIAKKYFFKKEVQQLRPHKSCIHQRE 334

RESULT 3
ADQ76696
ID ADQ76696 standard; protein; 334 AA.
XX ADQ76696;
XX 16-DEC-2004 (first entry)
XX Human kidney injury molecule-1 (KIM-1).
XX Human; KIM-1; kidney injury molecule-1; immunosuppressive; protozoacide;
KW muscular-gen.; neuroprotective; antianaemic; antithyroid; haemostatic;
KW antiallergic; antiinflammatory; vasotropic; nephrotropic.
XX Homo sapiens.
XX Key Location/Qualifiers
FT Peptide 1..20
FT Modified-site /label= Signal_peptide
FT Modified-site 65..67
FT Modified-site /note= "N-glycosylated"
FT Modified-site 258..260

FT /note= "N-glycosylated"
 FT 272. .274
 FT /note= "N-glycosylated"
 FT 286. .288
 FT /note= "N-glycosylated"
 FT 290. .311
 FT /note= "transmembrane domain"
 FT 324. .334
 FT /note= "C-terminal region unique to this splice variant"
 XX WO2004060041-A2.
 XX 22-JUL-2004.
 XX 29-DEC-2003; 2003WO-US041294.
 XX 30-DEC-2002; 2002US-0436934P.
 XX (BIOG-) BIOGEN IDEC MA INC.
 XX Rennert PD;
 XX WPI; 2004-534277/51.
 XX
 XX Use of a kidney injury molecule-1 (KIM-1) antagonist for e.g. treating
 PT Th2 cell-mediated diseases or inflammatory diseases, inhibiting B cell
 PT activation, or inhibiting production of a subset of antibodies against
 PT one or more antigens.
 XX
 PS Disclosure; SEQ ID NO 1; 68pp; English.
 XX
 CC The present sequence is that of human kidney injury molecule-1 (KIM-1), a
 CC type I cell membrane glycoprotein and member of the T cell immunoglobulin
 CC (Ig) and mucin domain (TIM) family. This protein has 334 amino acids or
 CC 359 amino acids ADO76690, depending on splice variation. It has been
 CC discovered that treatment of a mammal with a KIM-1 antagonist alters the
 CC interaction of T cells and other immune system cells, e.g. dendritic
 CC cells, monocytes, macrophages and B cells, and thereby strongly
 CC suppresses an IgG response to an antigen. Such treatment also eliminates
 CC IgG1 production by memory B cells in response to subsequent challenge
 CC with the antigen. Blockage of the binding of KIM-1 to its receptor
 CC reduces secretion of interferon-gamma by immune cells engaged in an
 CC antigen response in the mixed lymphocyte response assay. Based on these
 CC discoveries, the invention provides methods for therapeutically
 CC modulating immune function in autoimmune diseases and other disorders of
 CC the mammalian immune system. A method is claimed for inhibiting
 CC signalling between a T cell and a second cell, e.g. an antigen-presenting
 CC cell, in a mammal. The method involves identifying a mammal with an
 CC immune disease or disorder, or one preparing to receive a tissue graft,
 CC and administering a KIM-1 antagonist, especially a polypeptide
 CC comprising: a KIM-1 Ig domain, and lacking a transmembrane domain and a
 CC KIM-1 cytoplasmic domain; an anti-KIM-1 antibody; or an antigen-binding
 CC fragment of an anti-KIM-1 antibody. Preferably, the KIM-1 antagonist is a
 CC soluble polypeptide, which can include a KIM-1 mucin domain in addition
 CC to the KIM Ig domain, and may include a heterologous moiety such as an Fc
 CC moiety. The antagonist may be conjugated to a polymer such as
 CC polyethylene glycol. The KIM-1 antagonist is used in methods of:
 CC inhibiting activation of a B cell in a mammal; inhibiting disease relapse
 CC in an autoimmune disease; inhibiting epitope spreading in an autoimmune
 CC disease; treating a Th2 cell-mediated disease (e.g. myasthenia gravis,
 CC autoimmune haemolytic anemia, Chagas disease, Grave's disease,
 CC idiopathic thrombocytopenia purpura, Wegener's granulomatosis,
 CC polyarteritis nodosa, rapidly progressive crescentic glomerulonephritis,
 CC graft-versus-host disease, or systemic lupus nephritis) or inflammatory
 CC disease or disorder (e.g. inflammatory bowel diseases such as Crohn's
 CC disease, ulcerative colitis, and ileitis); and inhibiting secretion of
 CC IFN-gamma by lymphocytes.
 XX
 SQ Sequence 334 AA;
 Query Match 100.0%; Score 1749; DB 8; Length 334;
 Best Local Similarity 100.0%; Pred. No. 7.1e-118;
 Matches 334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHPQVWILSLILHLADSVAGSVKVGGEAGPSVTLPCHYSGAVTSMCNRSGCSLFTQNG 60
 DB 1 MHPQVWILSLILHLADSVAGSVKVGGEAGPSVTLPCHYSGAVTSMCNRSGCSLFTQNG 60
 QY 61 IYWTNGTHYTRKDTYKLLGDLRRDVSLLTIENTAVSDSGVYCCRVHRGNFNDMKITV 120
 DB 61 IYWTNGTHYTRKDTYKLLGDLRRDVSLLTIENTAVSDSGVYCCRVHRGNFNDMKITV 120
 QY 121 SLEIVPPKVTTPITVTTVTTRTSTVPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPTT 180
 DB 121 SLEIVPPKVTTPITVTTVTTRTSTVPTTTTPTTTTPTTTTPTTTTPTTTTPTT 180
 QY 181 TTTSVPTTTSIPTTTSVPVTTTSTVTFVPPMPLPRQNHPEVATSPSPQPAETHPTTLOGA 240
 DB 181 TTTSVPTTTSIPTTTSVPVTTTSTVTFVPPMPLPRQNHPEVATSPSPQPAETHPTTLOGA 240
 QY 241 IRREPTSSPLSYTTDNDTDTTSSDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 300
 DB 241 IRREPTSSPLSYTTDNDTDTTSSDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 300
 QY 301 VLLALGVIIIAKKYFFKKEVQQLRPHKSCIHORE 334
 DB 301 VLLALGVIIIAKKYFFKKEVQQLRPHKSCIHORE 334
 RESULT 4
 ABR58582
 ID ABR58582 standard; protein; 359 AA.
 XX ABR58582;
 AC ABR58582;
 XX 09-JUL-2003 (first entry)
 DT Human cancer related protein SEQ ID NO:239.
 XX Human cancer related protein SEQ ID NO:239.
 DE Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
 KW heart disease; atherosclerosis; endometriosis.
 KW Homo sapiens.
 OS WO2003025138-A2.
 PN 27-MAR-2003.
 XX 17-SEP-2002; 2002WO-US029560.
 PP 17-SEP-2001; 2001US-0323469P.
 PR 20-SEP-2001; 2001US-0323887P.
 PR 13-NOV-2001; 2001US-0350666P.
 PR 08-FEB-2002; 2002US-0355145P.
 PR 08-FEB-2002; 2002US-0355257P.
 PR 12-APR-2002; 2002US-0372246P.
 XX (EOSB-) EOS BIOTECHNOLOGY INC.
 PA Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
 PI Zlotnik A;
 XX WPI; 2003-354600/33.
 DR N-PSDB; ACC72709.
 XX New genes that are up-regulated or down-regulated in cancers, useful as
 PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
 PT therapeutic targets for screening drugs for treating these diseases.
 XX Claim 12; Page 742; 767pp; English.
 PS The present invention describes an isolated nucleic acid molecule, which
 CC comprises the sequence of any of the genes that are up-regulated or down-
 CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
 CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
 CC related gene nucleotide sequences which encode the proteins given in

CC ABR58521 to ABR58709. Also described: (1) determining the presence or
CC absence of a pathological cell in a patient; (2) an expression vector
CC comprising a nucleic acid molecule described above; (3) a host cell
CC comprising the vector; (4) an isolated polypeptide, which is encoded by
CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
CC of (4); (6) specifically targeting a compound to a pathological cell in a
CC patient by administering to the patient the antibody above; and (7) a
CC drug screening assay. The nucleic acid is useful as diagnostic markers or
CC therapeutic targets. In particular, the nucleic acid is useful for
CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
CC atherosclerosis and endometriosis. The nucleic acid is also useful in
CC drug screening, particularly for identifying agents for treating these
CC pathologies
XX
SQ Sequence 359 AA;

Query Match 96.3%; Score 1684; DB 6; Length 359;
Best Local Similarity 100.0%; Pred. No. 3.7e-113;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHPQVILSLILHLADSVAGSVKVGGEAGPSVTLPCHYSGAVTSMCNRGCSLFTCQNG 60
DB 1 MHPQVILSLILHLADSVAGSVKVGGEAGPSVTLPCHYSGAVTSMCNRGCSLFTCQNG 60
QY 61 IVWTNGTHVTYKDTYKLLGDLSDRRDVSLENTAVSDSGVCCRVHEHGFNDMKITV 120
DB 61 IVWTNGTHVTYKDTYKLLGDLSDRRDVSLENTAVSDSGVCCRVHEHGFNDMKITV 120
QY 121 SLEIVPPKVTTPITVTTVTVTSTVPTTTTPTTTTPTTTTPTTTTPTTTTPTTMTVS 180
DB 121 SLEIVPPKVTTPITVTTVTVTSTVPTTTTPTTTTPTTTTPTTTTPTTTTPTTMTVS 180
QY 181 TTTTSVPTTTSIPTTTSVPVTTTSTVFVPPMPLPRQNHPEVATSPSSQPAPETHPTTLOGA 240
DB 181 TTTTSVPTTTSIPTTTSVPVTTTSTVFVPPMPLPRQNHPEVATSPSSQPAPETHPTTLOGA 240
QY 241 IRREPTSSPLSYTTDGNDDVTSSDGLWNNNQTLFLEHSLLTANTTKGIYAGVCISVL 300
DB 241 IRREPTSSPLSYTTDGNDDVTSSDGLWNNNQTLFLEHSLLTANTTKGIYAGVCISVL 300
QY 301 VLLALLGVIIAKKYFFKKEVQQL 323
DB 301 VLLALLGVIIAKKYFFKKEVQQL 323

RESULT 5

ABP70438

ID ABP70438 standard; protein; 359 AA.

XX AC

XX ABP70438;

XX 22-APR-2003 (first entry)

DE Amino acid sequence of human TIM-1 allele 1.

XX T cell immunoglobulin domain; mucin domain; TIM; TIM-1; TIM-2; TIM-3;
KW TIM-4; immune dysfunction; chromosome 5; malignancy; allergy; eczema;
KW myelodysplastic syndrome; airway hyperreactivity; cancer; asthma;
KW allergic T cell response; autoimmune disease.

XX Homo sapiens.

OS WO2003002722-A2.

PN 09-JAN-2003.

PD 01-JUL-2002; 2002WO-US020890.

PF 29-JUN-2001; 2001US-0302344P.

PR (STRD) UNIV LELAND STANFORD JUNIOR.

XX McIntire JJ, Dekruyff RH, Umetsu DT, Freeman GJ, Kuchroo V;
PI WPI; 2003-210268/20.
XX N-ESDB; ABZ68332.
XX New nucleic acid comprising a mammalian T cell immunoglobulin domain and
PT mucin domain gene sequences, useful for treating cancer or asthma,
PT allergy, eczema or autoimmune disease.
XX Claim 10; Page 80-81; 94pp; English.
XX The present sequence is a human T cell immunoglobulin domain and mucin
CC domain-1 (TIM-1) polypeptide. The specification describes TIM-1, TIM-2,
CC TIM-3 and TIM-4. TIM polypeptides are cell surface molecules with
CC conserved IgV and mucin domains. The locus comprising the TIM family is
CC genetically associated with immune dysfunction, including asthma. The TIM
CC gene family is located within a region of human chromosome 5 that is
CC commonly deleted in malignancies and myelodysplastic syndrome. Variants
CC of TIM-1 and TIM-3 are associated with susceptibility to airway
CC hyperreactivity and allergic T cell responses, and other variants
CC associated with protection against these responses. T cells express TIM
CC proteins, which critically regulate CD4 T cell differentiation. Th1 cells
CC preferentially express TIM-3, while Th2 cells preferentially express TIM-
CC 1. TIM polypeptides and polynucleotides are useful for treating cancer,
CC asthma, allergies, eczema or autoimmune diseases
XX
SQ Sequence 359 AA;

Query Match 96.3%; Score 1684; DB 6; Length 359;
Best Local Similarity 100.0%; Pred. No. 3.7e-113;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHPQVILSLILHLADSVAGSVKVGGEAGPSVTLPCHYSGAVTSMCNRGCSLFTCQNG 60
DB 1 MHPQVILSLILHLADSVAGSVKVGGEAGPSVTLPCHYSGAVTSMCNRGCSLFTCQNG 60
QY 61 IVWTNGTHVTYKDTYKLLGDLSDRRDVSLENTAVSDSGVCCRVHEHGFNDMKITV 120
DB 61 IVWTNGTHVTYKDTYKLLGDLSDRRDVSLENTAVSDSGVCCRVHEHGFNDMKITV 120
QY 121 SLEIVPPKVTTPITVTTVTVTSTVPTTTTPTTTTPTTTTPTTTTPTTTTPTTMTVS 180
DB 121 SLEIVPPKVTTPITVTTVTVTSTVPTTTTPTTTTPTTTTPTTTTPTTTTPTTMTVS 180
QY 181 TTTTSVPTTTSIPTTTSVPVTTTSTVFVPPMPLPRQNHPEVATSPSSQPAPETHPTTLOGA 240
DB 181 TTTTSVPTTTSIPTTTSVPVTTTSTVFVPPMPLPRQNHPEVATSPSSQPAPETHPTTLOGA 240
QY 241 IRREPTSSPLSYTTDGNDDVTSSDGLWNNNQTLFLEHSLLTANTTKGIYAGVCISVL 300
DB 241 IRREPTSSPLSYTTDGNDDVTSSDGLWNNNQTLFLEHSLLTANTTKGIYAGVCISVL 300
QY 301 VLLALLGVIIAKKYFFKKEVQQL 323
DB 301 VLLALLGVIIAKKYFFKKEVQQL 323

RESULT 6

ABR48174

ID ABR48174 standard; protein; 359 AA.

XX AC

XX ABR48174;

XX 12-JUN-2003 (first entry)

XX Human bladder cancer associated protein sequence SEQ ID NO:64.

XX Human; bladder cancer; cytostatic; gene therapy; vaccine.

XX Homo sapiens.

XX OS

XX WO2003003906-A2.

XX 16-JAN-2003.
PD
XX
PF
XX
XX
XX
PR
03-JUL-2002; 2002WO-US021338.
XX
PR
03-JUL-2001; 2001US-0302814P.
XX
PR
03-AUG-2001; 2001US-0310099P.
XX
PR
08-NOV-2001; 2001US-0343705P.
XX
PR
13-NOV-2001; 2001US-0350666P.
XX
PR
12-APR-2002; 2002US-0372246P.
XX
XX
PA
(EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX
PI
Mack DH, Aziz N;
XX
XX
DR
WPI; 2003-201532/19.
XX
DR
N-PSDB; ACC50985.
XX
XX
PT
Detecting a bladder cancer-associated transcript in a cell from a
PT
patient, comprises contacting a biological sample from the patient with a
PT
bladder cancer-associated polynucleotide or antibody.
XX
XX
PS
Claim 10; Page 252; 307pp; English.
XX
XX
CC
The present invention describes a method for detecting a bladder cancer-
CC
associated transcript in a cell from a patient. The method comprises
CC
contacting a biological sample from the patient with a polynucleotide
CC
that selectively hybridizes to a sequence that is 80 % identical to a
CC
table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059
CC
encode the human bladder cancer-associated proteins given in ABR48146 to
CC
ABR48242). Bladder cancer-associated sequences from the present invention
CC
have cytostatic activities, and can be used in antisense gene therapy and
CC
in vaccine production. The method can be used for detecting a bladder
CC
cancer-associated transcript in a cell from a patient. The method is
CC
useful in diagnosing or treating bladder cancer and in screening for
CC
compounds that modulate bladder cancer, such as hormones or antibodies.
CC
The nucleic acid molecules from the present invention may be used in
CC
various screening and diagnostic methods, and for gene therapy, vaccine
CC
and/or antisense/inhibition applications
XX
XX
SQ
Sequence 359 AA;
Query Match 96.3%; Score 1684; DB 6; Length 359;
Best Local Similarity 100.0%; Pred. No. 3.7e-113;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHPQVILSLIHLADSVAGSVKVGEGAPSVTLPCHYSGAVTSMCWNRGCSLFTCQNG 60
DB 1 MHPQVILSLIHLADSVAGSVKVGEGAPSVTLPCHYSGAVTSMCWNRGCSLFTCQNG 60
QY 61 IVWTNGTHVTRKDYKLLGLSRDVSLLTIENTAVSDSGVYCCVHRGFNMDKITV 120
DB 61 IVWTNGTHVTRKDYKLLGLSRDVSLLTIENTAVSDSGVYCCVHRGFNMDKITV 120
QY 121 SLEIVPPKVTTPPIVTTVPTVTRTSTVPTTTTPTVPTTMSIPTTTTPTTMTVS 180
DB 121 SLEIVPPKVTTPPIVTTVPTVTRTSTVPTTTTPTVPTTMSIPTTTTPTTMTVS 180
QY 181 TTSVPTTTSIPTTTSVPVPTTSTVFPMPMLPRQNHPEVATSPSPQPAETHPTTLOQA 240
DB 181 TTSVPTTTSIPTTTSVPVPTTSTVFPMPMLPRQNHPEVATSPSPQPAETHPTTLOQA 240
QY 241 IRREPTSSPLSYTTDGNDDVTESDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 300
DB 241 IRREPTSSPLSYTTDGNDDVTESDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 300
QY 301 VLLALLGVIIIAKKYFFKKEVQQL 323
DB 301 VLLALLGVIIIAKKYFFKKEVQQL 323
RESULT 7
AAO26680

AAO26680 standard; protein; 359 AA.
AAO26680;
20-MAR-2003 (first entry)
KIM-1 related protein, SEQ ID No 8.
Cytostatic; gene therapy; antibody; antigen; antigen-binding;
proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;
renal disease; injury; renal cancer; human.
Homo sapiens.
WO200298920-A1.
12-DEC-2002.
31-MAY-2002; 2002WO-US017402.
01-JUN-2001; 2001US-0295449P.
04-JUN-2001; 2001US-0295907P.
(BIOJ) BIOGEN INC.
(GEO) GEN HOSPITAL CORP.
Bailey V, Bonventre J;
WPI; 2003-156845/15.
New antibody, antibody derivative or antigen-binding polypeptide that
inhibits proteolytic release of a soluble kidney injury molecule-1
polypeptide, useful for treating or preventing renal disease or injury,
e.g. renal cancer.
Disclosure; Page 40-41; 42pp; English.
The invention relates to a novel antibody, antibody derivative or antigen
-binding polypeptide that inhibits proteolytic release of a soluble
kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.
The antibody, antibody derivative or antigen-binding polypeptide is
useful for treating or preventing renal disease or injury, e.g. renal
cancer. The antibody is also useful for inhibiting shedding of the KIM-1
polypeptide. This sequence represents a protein relating to the KIM-1
protein of the invention
SQ
Sequence 359 AA;
Query Match 96.3%; Score 1684; DB 6; Length 359;
Best Local Similarity 100.0%; Pred. No. 3.7e-113;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHPQVILSLIHLADSVAGSVKVGEGAPSVTLPCHYSGAVTSMCWNRGCSLFTCQNG 60
DB 1 MHPQVILSLIHLADSVAGSVKVGEGAPSVTLPCHYSGAVTSMCWNRGCSLFTCQNG 60
QY 61 IVWTNGTHVTRKDYKLLGLSRDVSLLTIENTAVSDSGVYCCVHRGFNMDKITV 120
DB 61 IVWTNGTHVTRKDYKLLGLSRDVSLLTIENTAVSDSGVYCCVHRGFNMDKITV 120
QY 121 SLEIVPPKVTTPPIVTTVPTVTRTSTVPTTTTPTVPTTMSIPTTTTPTTMTVS 180
DB 121 SLEIVPPKVTTPPIVTTVPTVTRTSTVPTTTTPTVPTTMSIPTTTTPTTMTVS 180
QY 181 TTSVPTTTSIPTTTSVPVPTTSTVFPMPMLPRQNHPEVATSPSPQPAETHPTTLOQA 240
DB 181 TTSVPTTTSIPTTTSVPVPTTSTVFPMPMLPRQNHPEVATSPSPQPAETHPTTLOQA 240
QY 241 IRREPTSSPLSYTTDGNDDVTESDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 300
DB 241 IRREPTSSPLSYTTDGNDDVTESDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 300
QY 301 VLLALLGVIIIAKKYFFKKEVQQL 323

Db	301	VLLALLGVIIIAKYPFKKEVQQL 323	
RESULT 8			
AD36594			
ID	AD36594	standard; protein; 359 AA.	
AC	AD36594;		
XX			
DT	29-JAN-2004	(first entry)	
DE	Human NOV1b protein SEQ ID NO:4.		
XX			
KW	human; NOVX; cytostatic; antiinflammatory; gene therapy; vaccine;		
KW	renal cancer; inflammation; tissue typing.		
OS	Homo sapiens.		
XX			
PN	WO2003080856-A2.		
XX			
PD	02-OCT-2003.		
PF	19-MAR-2003; 2003WO-US008490.		
XX			
PR	19-MAR-2002; 2002US-0365491P.		
PR	13-SEP-2002; 2002US-0410618P.		
XX			
PA	(CURA-) CURAGEN CORP.		
XX			
PI	Lepley DM, Rieger DK, Tse K, Rastelli L, Smithson G, Mesri M;		
PI	Ooi CE, Anderson DW, Guo X, Giot L, Starling G;		
XX			
DR	WPI; 2003-876927/81.		
DR	N-PSDB; ADE36593.		
XX			
PT	New polypeptide, useful for preparing a composition for treating or		
PT	preventing a pathology associated with NOVX polypeptide e.g. renal cancer		
PT	or inflammation, or for tissue typing.		
XX			
PS	Claim 1; SEQ ID NO 4; 239pp; English.		
XX			
CC	The present invention describes an isolated human NOVX polypeptide, where		
CC	X is la to ld or 2a to 2h, or its mature form, a sequence that is at		
CC	least 95 % identical to it, or a sequence comprising one or more		
CC	conservative substitutions in the amino acid sequence. The NOVX		
CC	polypeptide, and nucleic acid sequence encoding it, has cytostatic and		
CC	antiinflammatory activities, and can be used in gene therapy, and in		
CC	vaccines. The NOVX polypeptide is useful for preparing a composition for		
CC	treating or preventing a pathology associated with NOVX polypeptide e.g.		
CC	renal cancer or inflammation, or for tissue typing. The present sequence		
CC	represents human NOV1b from the present invention.		
XX			
SQ	Sequence 359 AA;		
Query Match	96.3 %; Score 1684; DB 7; Length 359;		
Best Local Similarity	100.0 %; Pred. No. 3.7e-113; Mismatches 0; Gaps 0;		
Matches 323; Conservative	0; Indels		
QY	1	MHPQVVILSLIHLADSVAGSVKVGEGAPSVTLFCHYSGAVTSCMNRGCSLFTCCQNG 60	
Db	1	MHPQVVILSLIHLADSVAGSVKVGEGAPSVTLFCHYSGAVTSCMNRGCSLFTCCQNG 60	
QY	61	IWTNGTHVTRKOTRYKLLGLDLSRRDVSLLTIENTAVSDSGVYCCRVHRGFNDMKITV 120	
Db	61	IWTNGTHVTRKOTRYKLLGLDLSRRDVSLLTIENTAVSDSGVYCCRVHRGFNDMKITV 120	
QY	121	SLEIVPDKVTTPVITVPTVTSTVPTTTPVTPTTPTTMSIPTTTVPTMTVS 180	
Db	121	SLEIVPDKVTTPVITVPTVTSTVPTTTPVTPTTPTTMSIPTTTVPTMTVS 180	
QY	181	TTTTSVPTTTSIPTTTSTVPVTTTSTVPVPMPLPRQNHEPVATSPSSPQPAETHPTTLOGA 240	

Db	181	TTTTSVPTTTSIPTTTSTVPVTTTSTVPVPMPLPRQNHEPVATSPSSPQPAETHPTTLOGA 240	
QY	241	IRREPTSSPLYSYTTDGNDFVTTESDGLWNNNOTQLFLEHSLLTANTTTKGIYAGVCISVL 300	
Db	241	IRREPTSSPLYSYTTDGNDFVTTESDGLWNNNOTQLFLEHSLLTANTTTKGIYAGVCISVL 300	
QY	301	VLLALLGVIIIAKYPFKKEVQQL 323	
Db	301	VLLALLGVIIIAKYPFKKEVQQL 323	
RESULT 9			
ADN38984			
ID	ADN38984	standard; protein; 359 AA.	
XX			
AC	ADN38984;		
XX			
DT	17-JUN-2004	(first entry)	
XX			
DE	Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:302.		
XX			
KW	Human; differential expression; cancer; angiogenic disorder;		
KW	fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;		
KW	inflammatory disease; autoimmune disease;		
KW	retinal neovascularisation syndrome; scarring; uterine fibroid;		
KW	detection; diagnosis; prognosis; drug screening; drug targeting;		
KW	wound healing; contraception; cytostatic; cardiant; immunomodulatory;		
XX			
OS	Homo sapiens.		
XX			
PN	WO2003042661-A2.		
XX			
PD	22-MAY-2003.		
XX			
PF	13-NOV-2002; 2002WO-US036810.		
XX			
PR	13-NOV-2001; 2001US-0350666P.		
PR	21-NOV-2001; 2001US-032464P.		
PR	29-NOV-2001; 2001US-0334393P.		
PR	03-DEC-2001; 2001US-0335394P.		
PR	14-DEC-2001; 2001US-0340376P.		
PR	08-JAN-2002; 2002US-0347211P.		
PR	10-JAN-2002; 2002US-0347349P.		
PR	13-FEB-2002; 2002US-0356714P.		
PR	20-FEB-2002; 2002US-0359077P.		
PR	29-MAR-2002; 2002US-0368809P.		
PR	04-APR-2002; 2002US-0370110P.		
PR	12-APR-2002; 2002US-0372246P.		
PR	16-JUL-2002; 2002US-0396839P.		
PR	22-JUL-2002; 2002US-0397755P.		
PR	09-SEP-2002; 2002US-0409450P.		
XX			
PA	(EOSB-) EOS BIOTECHNOLOGY INC.		
XX			
PI	Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;		
PI	Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;		
XX			
DR	WPI; 2003-468649/44.		
DR	N-PSDB; ADN38983.		
XX			
PT	Determining the presence or absence of a pathological cell in a patient,		
PT	useful for diagnosing, prognosing or treating cancer, comprises detecting		
PT	a nucleic acid in a biological sample.		
XX			
PS	Claim 12; SEQ ID NO 302; 1385pp; English.		
XX			
CC	The invention relates to nucleic acids and proteins (ADN38683-ADN40064)		
CC	whose expression is upregulated or downregulated in specific cancers or		
CC	other diseases such as angiogenic or fibrotic disorders, and to methods		

CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularisation syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a polypeptide of the invention.

XX
SQ

Query Match 96.3%; Score 1684; DB 7; Length 359;
Best Local Similarity 100.0%; Pred. No. 3.7e-113;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHPQVILSLILHLADSVAGSVKVGEGAPSVTLPCYSGAVTSMCMNRGSCSLFTCQNG 60

DB 1 MHPQVILSLILHLADSVAGSVKVGEGAPSVTLPCYSGAVTSMCMNRGSCSLFTCQNG 60

QY 61 IVWNGTHVTRKDYKLLGDLRRDVSLLTIENTAVSDSGVYCCRVHRGWFNDMKITV 120

DB 61 IVWNGTHVTRKDYKLLGDLRRDVSLLTIENTAVSDSGVYCCRVHRGWFNDMKITV 120

QY 121 SLEIVPPKVTTPPIVNTVPTVTRTSITVPTTPTTPTTPTTPTTPTTPTTPTTPTT 180

DB 121 SLEIVPPKVTTPPIVNTVPTVTRTSITVPTTPTTPTTPTTPTTPTTPTTPTTPTT 180

QY 181 TTTSVPTTTSIPTTSVPVTTTSTVTPMPPLPRQNHPEVATSPSPQPAETHPTTLOQA 240

DB 181 TTTSVPTTTSIPTTSVPVTTTSTVTPMPPLPRQNHPEVATSPSPQPAETHPTTLOQA 240

QY 241 IRREPTSPLYSYTTDNDPTVTESSDGLWNNNQTLFLEHSLLTANTTKGIYAGVCISYL 300

DB 241 IRREPTSPLYSYTTDNDPTVTESSDGLWNNNQTLFLEHSLLTANTTKGIYAGVCISYL 300

QY 301 VLLALGLVILIAKKYFKKXVQQL 323

DB 301 VLLALGLVILIAKKYFKKXVQQL 323

RESULT 10

ID ADQ76690 standard; protein; 359 AA.

XX

AC ADQ76690;

XX 16-DEC-2004 (first entry)

XX Human kidney injury molecule-1 (KIM-1).

XX Human; KIM-1; kidney injury module-1; immunosuppressive; protozoacide;
KW muscular-gen.; neuroprotective; antianemic; antithyroid; haemostatic;
KW antiallergic; antiinflammatory; vasotropic; nephropic.

OS Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..20

FT Modified-site /label= Signal_peptide

FT Modified-site /note= "N-glycosylated"

FT Modified-site /note= "N-glycosylated"

FT Modified-site /note= "N-glycosylated"

FT Modified-site /note= "N-glycosylated"

FT Domain 290..311
FT Region /note= "Transmembrane domain"
FT 324..359
XX /note= "C-terminal region unique to this splice variant"
PN WO2004060041-A2.

XX 22-JUL-2004.

XX 29-DEC-2003; 2003WO-US041294.

XX 30-DEC-2002; 2002US-0436934P.

XX (BIOG-) BIOGEN IDEC MA INC.

XX Remmert PD;

XX WPI; 2004-534277/51.

XX Use of a kidney injury molecule-1 (KIM-1) antagonist for e.g. treating
XX Th2 cell-mediated diseases or inflammatory diseases, inhibiting B cell
XX activation, or inhibiting production of a subset of antibodies against
XX one or more antigens.

XX Disclosure; SEQ ID NO 1; 69pp; English.

XX The present sequence is that of human kidney injury molecule-1 (KIM-1), a
XX type I cell membrane glycoprotein and member of the T cell immunoglobulin
XX (Ig) and mucin domain (TIM) family. This protein has 334 amino acids
XX ADQ76696 or 359 amino acids, depending on splice variation. It has been
XX discovered that treatment of a mammal with a KIM-1 antagonist alters the
XX interaction of T cells and other immune system cells, e.g. dendritic
XX cells, monocytes, macrophages and B cells, and thereby strongly
XX suppresses an Ig response to an antigen. Such treatment also eliminates
XX IgG1 production by memory B cells in response to subsequent challenge
XX with the antigen. Blockage of the binding of KIM-1 to its receptor
XX reduces secretion of interferon-gamma by immune cells engaged in an
XX antigen response in the mixed lymphocyte response assay. Based on these
XX discoveries, the invention provides methods for therapeutically
XX modulating immune function in autoimmune diseases and other disorders of
XX the mammalian immune system. A method is claimed for inhibiting
XX signalling between a T cell and a second cell, e.g. an antigen-presenting
XX cell, in a mammal. The method involves identifying a mammal with an
XX immune disease or disorder, or one preparing to receive a tissue graft,
XX and administering a KIM-1 antagonist, especially a polypeptide
XX comprising: a KIM-1 Ig domain, and lacking a transmembrane domain and a
XX KIM-1 cytoplasmic domain; an anti-KIM-1 antibody; or an antigen-binding
XX fragment of an anti-KIM-1 antibody. Preferably, the KIM-1 antagonist is a
XX soluble polypeptide, which can include a KIM-1 mucin domain in addition
XX to the KIM Ig domain, and may include a heterologous moiety such as an Fc
XX moiety. The antagonist may be conjugated to a polymer such as
XX polyethylene glycol. The KIM-1 antagonist is used in methods of:
XX inhibiting activation of a B cell in a mammal; inhibiting disease relapse
XX in an autoimmune disease; inhibiting epicope spreading in an autoimmune
XX disease; treating a Th2 cell-mediated disease (e.g. myasthenia gravis,
XX autoimmune haemolytic anaemia, Chagas disease, Grave's disease,
XX idiopathic thrombocytopenia purpura, Wegener's granulomatosis,
XX polyarteritis nodosa, rapidly progressive crescentic glomerulonephritis,
XX graft-versus-host disease, or systemic lupus nephritis) or inflammatory
XX disease or disorder (e.g. inflammatory bowel diseases such as Crohn's
XX disease, ulcerative colitis, and ileitis); and inhibiting secretion of
XX IFN-gamma by lymphocytes.

XX Sequence 359 AA;

Query Match 96.3%; Score 1684; DB 8; Length 359;
Best Local Similarity 100.0%; Pred. No. 3.7e-113;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHPQVILSLILHLADSVAGSVKVGEGAPSVTLPCYSGAVTSMCMNRGSCSLFTCQNG 60

DB 1 MHPQVILSLILHLADSVAGSVKVGEGAPSVTLPCYSGAVTSMCMNRGSCSLFTCQNG 60

XX PT New nucleic acid comprising a mammalian T cell immunoglobulin domain and
 PT Mucin domain gene sequences, useful for treating cancer or asthma,
 PT allergy, eczema or autoimmune disease.
 XX PS Claim 10; Page 84-85; 94pp; English.
 XX CC The present sequence is a human T cell immunoglobulin domain and mucin
 CC domain-1 (TIM-1) polypeptide. The specification describes TIM-1, TIM-2,
 CC TIM-3 and TIM-4. TIM polypeptides are cell surface molecules with
 CC conserved IgV and mucin domains. The locus comprising the TIM family is
 CC genetically associated with immune dysfunction, including asthma. The TIM
 CC gene family is located within a region of human chromosome 5 that is
 CC commonly deleted in malignancies and myelodysplastic syndrome. Variants
 CC of TIM-1 and TIM-3 are associated with susceptibility to airway
 CC hyperactivity and allergic T cell responses, and other variants
 CC associated with protection against these responses. T cells express TIM
 CC proteins, which critically regulate CD4 T cell differentiation. Th1 cells
 CC preferentially express TIM-3, while Th2 cells preferentially express TIM-
 CC 1. TIM polypeptides and polynucleotides are useful for treating cancer,
 CC asthma, allergies, eczema or autoimmune diseases
 XX PS Sequence 359 AA;
 CC Query Match 95.5%; Score 1671; DB 6; Length 359;
 CC Best Local Similarity 99.1%; Pred. No. 3.2e-112;
 CC Matches 320; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MHPQVILSLIHLADSVAGSVKVGEGAPSVTLPCHYSGAVTSMCNRGSCSLFTCQNG 60
 DB 1 MHPQVILSLIHLADSVAGSVKVGEGAPSVTLPCHYSGAVTSMCNRGSCSLFTCQNG 60
 QY 61 IVWTNGTHVTRKOTRYKLLGLDLSRDDVSLTIENTAVSDSGVYCCRVHRGFNDMKITV 120
 DB 61 IVWTNGTHVTRKOTRYKLLGLDLSRDDVSLTIENTAVSDSGVYCCRVHRGFNDMKITV 120
 QY 121 SLEIVPPKVTTPPIVTTVTPTVTTRTSTTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 180
 DB 121 SLEIVPPKVTTPPIVTTVTPTVTTRTSTTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 180
 QY 181 TTTSVPTTTSIPPTTSVPVTTTSTVTPVPMPLPRQNHPEVATSPSPQPAETHPTTLOGA 240
 DB 181 TTTSVPTTTSIPPTTSVPVTTTSTVTPVPMPLPRQNHPEVATSPSPQPAETHPTTLOGT 240
 QY 241 IRREPTSSPLSYTTDGNVTVESSDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 300
 DB 241 IRREPTSSPLSYTTDGNVTVESSDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 300
 QY 301 VLLALLGVIIAKKYFFKKEVQQL 323
 DB 301 VLLALLGVIIAKKYFFKKEVQQL 323
 RESULT 13
 ABP70440
 ID ABP70440 standard; protein; 365 AA.
 XX AC ABP70440;
 DT 22-APR-2003 (first entry)
 DE Amino acid sequence of human TIM-1 allele 3.
 DE T cell immunoglobulin domain; mucin domain; TIM; TIM-1; TIM-2; TIM-3;
 KW TIM-4; immune dysfunction; chromosome 5; malignancy; allergy; eczema;
 KW myelodysplastic syndrome; airway hyperactivity; cancer; asthma;
 KW allergic T cell response; autoimmune disease.
 XX OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Misc-difference 208
 FT /note= "encoded by RCG"

XX WO2003002722-A2.
 XX 09-JAN-2003.
 XX 01-JUL-2002; 2002WO-US020890.
 XX 29-JUN-2001; 2001US-0302344P.
 XX (STRD) UNIV LELAND STANFORD JUNIOR.
 XX McIntire JJ, Dekruffy RH, Umetsu DT, Freeman GJ, Kuchroo V;
 XX WPI; 2003-210268/20.
 XX N-PSDB; ABZ68334.
 XX New nucleic acid comprising a mammalian T cell immunoglobulin domain and
 PT Mucin domain gene sequences, useful for treating cancer or asthma,
 PT allergy, eczema or autoimmune disease.
 XX Claim 10; Page 83-84; 94pp; English.
 CC The present sequence is a human T cell immunoglobulin domain and mucin
 CC domain-1 (TIM-1) polypeptide. The specification describes TIM-1, TIM-2,
 CC TIM-3 and TIM-4. TIM polypeptides are cell surface molecules with
 CC conserved IgV and mucin domains. The locus comprising the TIM family is
 CC genetically associated with immune dysfunction, including asthma. The TIM
 CC gene family is located within a region of human chromosome 5 that is
 CC commonly deleted in malignancies and myelodysplastic syndrome. Variants
 CC of TIM-1 and TIM-3 are associated with susceptibility to airway
 CC hyperactivity and allergic T cell responses, and other variants
 CC associated with protection against these responses. T cells express TIM
 CC proteins, which critically regulate CD4 T cell differentiation. Th1 cells
 CC preferentially express TIM-3, while Th2 cells preferentially express TIM-
 CC 1. TIM polypeptides and polynucleotides are useful for treating cancer,
 CC asthma, allergies, eczema or autoimmune diseases
 XX PS Sequence 365 AA;
 CC Query Match 95.3%; Score 1666; DB 6; Length 365;
 CC Best Local Similarity 97.9%; Pred. No. 7.5e-112;
 CC Matches 322; Conservative 0; Mismatches 1; Indels 6; Gaps 1;
 QY 1 MHPQVILSLIHLADSVAGSVKVGEGAPSVTLPCHYSGAVTSMCNRGSCSLFTCQNG 60
 DB 1 MHPQVILSLIHLADSVAGSVKVGEGAPSVTLPCHYSGAVTSMCNRGSCSLFTCQNG 60
 QY 61 IVWTNGTHVTRKOTRYKLLGLDLSRDDVSLTIENTAVSDSGVYCCRVHRGFNDMKITV 120
 DB 61 IVWTNGTHVTRKOTRYKLLGLDLSRDDVSLTIENTAVSDSGVYCCRVHRGFNDMKITV 120
 QY 121 SLEIVPPKVTTPPIVTTVTPTVTTRTSTTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 174
 DB 121 SLEIVPPKVTTPPIVTTVTPTVTTRTSTTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 180
 QY 175 TTMTVSTTTSVPTTTSIPPTTSVPVTTTSTVTPVPMPLPRQNHPEVATSPSPQPAETHP 234
 DB 181 TTMTVSTTTSVPTTTSIPPTTSVPVTTTSTVTPVPMPLPRQNHPEVATSPSPQPAETHP 240
 QY 235 TTLOGAIRREPTSSPLSYTTDGNVTVESSDGLWNNQTLFLEHSLLTANTTKGIYAG 294
 DB 241 TTLOGAIRREPTSSPLSYTTDGNVTVESSDGLWNNQTLFLEHSLLTANTTKGIYAG 300
 QY 295 VCISVLVLLALLGVIIAKKYFFKKEVQQL 323
 DB 301 VCISVLVLLALLGVIIAKKYFFKKEVQQL 329
 RESULT 14
 ABP70442
 ID ABP70442 standard; protein; 364 AA.
 XX AC ABP70442;

XX 22-APR-2003 (first entry)
DT Amino acid sequence of human TIM-1 allele 5.
XX
XX T cell immunoglobulin domain; mucin domain; TIM; TIM-1; TIM-2; TIM-3;
KW TIM-4; immune dysfunction; chromosome 5; malignancy; allergy; eczema;
KW myelodysplastic syndrome; airway hyperreactivity; cancer; asthma;
KW allergic T cell response; autoimmune disease.
XX
OS Homo sapiens.
XX
XX WO2003002722-A2.
PN
XX
XX 09-JAN-2003.
XX
XX 01-JUL-2002; 2002WO-US020890.
PF
XX 29-JUN-2001; 2001US-0302344P.
PR
XX (STRD) UNIV LELAND STANFORD JUNIOR.
PA
XX
XX McIntire JJ, Dekruyff RH, Umetsu DT, Freeman GJ, Kuchroo V;
PI
XX WPI; 2003-210268/20.
DR
XX N-PSDB; ABZ68336.
DR
XX New nucleic acid comprising a mammalian T cell immunoglobulin domain and
FT Mucin domain gene sequences, useful for treating cancer or asthma,
PT allergy, eczema or autoimmune disease.
PT
XX
XX Claim 10; Page 86-87; 94pp; English.
PS
XX
XX The present sequence is a human T cell immunoglobulin domain and mucin
CC domain-1 (TIM-1) polypeptide. The specification describes TIM-1, TIM-2,
CC TIM-3 and TIM-4. TIM polypeptides are cell surface molecules with
CC conserved IgV and mucin domains. The locus comprising the TIM family is
CC genetically associated with immune dysfunction, including asthma. The TIM
CC gene family is located within a region of human chromosome 5 that is
CC commonly deleted in malignancies and myelodysplastic syndrome. Variants
CC of TIM-1 and TIM-3 are associated with susceptibility to airway
CC hyperreactivity and allergic T cell responses, and other variants
CC associated with protection against these responses. T cells express TIM
CC proteins, which critically regulate CD4 T cell differentiation. Th1 cells
CC preferentially express TIM-3, while Th2 cells preferentially express TIM-
CC 1. TIM polypeptides and polynucleotides are useful for treating cancer,
CC asthma, allergies, eczema or autoimmune diseases
XX
XX Sequence 364 AA;
PS
XX
XX Query Match 94.7%; Score 1655.5; DB 6; Length 364;
Best Local Similarity 97.9%; Pred. No. 4.3e-111;
Matches 322; Conservative 0; Mismatches 0; Indels 7; Gaps 2;
QY 1 MHPQVILSLIHLADSVAGSVKVGGEAGPSVTLPCYSGAVTSCWNRGSCSLFTCCQNG 60
DB 1 MHPQVILSLIHLADSVAGSVKVGGEAGPSVTLPCYSGAVTSCWNRGSCSLFTCCQNG 60
QY 61 IVWTNGTHVTRKDTYKLLGLDLSRRDVSLLTIENTAVSDSGVYCCRVHRGWFNDMKITV 120
DB 61 IVWTNGTHVTRKDTYKLLGLDLSRRDVSLLTIENTAVSDSGVYCCRVHRGWFNDMKITV 120
QY 121 SLEIYPPKVTTPITVTTVTVTVTSTVTPT-----TTTTVTVTVTPTTTSIPTTTTVP 174
DB 121 SLEIYPPKVTTPITVTTVTVTVTSTVTPT-----TTTTVTVTVTPTTTSIPTTTTVP 180
QY 175 TMTVSTTTSPTTTSIPTTSPVTTTSTVTPVPMPLPRQNHVPATSPSPQPAETHP 234
DB 181 TMTVSTTTSPTTTSIPTTSPVTTTSTVTPVPMPLPRQNHVPATSPSPQPAETHP 239
QY 235 TTLOGAIRREPTSSPLSYTTDGNVTETSSDGLWNNNQTLFLEHSLLTANTTKGIYAG 294
DB 240 TTLOGAIRREPTSSPLSYTTDGNVTETSSDGLWNNNQTLFLEHSLLTANTTKGIYAG 299

QY 295 VCISVLVLLALLGVIIAKKYFFKKEVQQL 323
DB 300 VCISVLVLLALLGVIIAKKYFFKKEVQQL 328
RESULT 15
ABP70443
ID ABP70443 standard; protein; 364 AA.
XX
XX AC ABP70443;
XX
XX 22-APR-2003 (first entry)
XX
XX Amino acid sequence of human TIM-1 allele 6.
XX
XX T cell immunoglobulin domain; mucin domain; TIM; TIM-1; TIM-2; TIM-3;
KW TIM-4; immune dysfunction; chromosome 5; malignancy; allergy; eczema;
KW myelodysplastic syndrome; airway hyperreactivity; cancer; asthma;
KW allergic T cell response; autoimmune disease.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 123 /note= "encoded by GAG"
FT
FT Misc-difference 161 /note= "encoded by GACT"
FT
FT Misc-difference 201 /note= "encoded by ACAAGT"
FT
XX WO2003002722-A2.
XX
XX 09-JAN-2003.
XX
XX 01-JUL-2002; 2002WO-US020890.
XX
XX 29-JUN-2001; 2001US-0302344P.
XX
XX (STRD) UNIV LELAND STANFORD JUNIOR.
XX
XX McIntire JJ, Dekruyff RH, Umetsu DT, Freeman GJ, Kuchroo V;
PI
XX WPI; 2003-210268/20.
DR
XX N-PSDB; ABZ68336.
DR
XX New nucleic acid comprising a mammalian T cell immunoglobulin domain and
FT Mucin domain gene sequences, useful for treating cancer or asthma,
PT allergy, eczema or autoimmune disease.
PT
XX
XX Claim 10; Page 87-88; 94pp; English.
PS
XX
XX The present sequence is a human T cell immunoglobulin domain and mucin
CC domain-1 (TIM-1) polypeptide. The specification describes TIM-1, TIM-2,
CC TIM-3 and TIM-4. TIM polypeptides are cell surface molecules with
CC conserved IgV and mucin domains. The locus comprising the TIM family is
CC genetically associated with immune dysfunction, including asthma. The TIM
CC gene family is located within a region of human chromosome 5 that is
CC commonly deleted in malignancies and myelodysplastic syndrome. Variants
CC of TIM-1 and TIM-3 are associated with susceptibility to airway
CC hyperreactivity and allergic T cell responses, and other variants
CC associated with protection against these responses. T cells express TIM
CC proteins, which critically regulate CD4 T cell differentiation. Th1 cells
CC preferentially express TIM-3, while Th2 cells preferentially express TIM-
CC 1. TIM polypeptides and polynucleotides are useful for treating cancer,
CC asthma, allergies, eczema or autoimmune diseases
XX
XX Sequence 364 AA;
PS
XX
XX Query Match 94.0%; Score 1643.5; DB 6; Length 364;
Best Local Similarity 97.3%; Pred. No. 3.1e-110;
Matches 320; Conservative 1; Mismatches 1; Indels 7; Gaps 2;

Qy	1	MHPQVILSLILHLADSVAGSVKVGGEAGPSVTLPCHYSGAVTSMCWNRGSCSLFTCQNG	60
Db	1	MHPQVILSLILHLADSVAGSVKVGGEAGPSVTLPCHYSGAVTSMCWNRGSCSLFTCQNG	60
Qy	61	IWVTNGTHVYRKDTRYKLLGDLRRDVSLLTIENTAVSDSGVYCCRVHRGWENDMKITV	120
Db	61	IWVTNGTHVYRKDTRYKLLGDLRRDVSLLTIENTAVSDSGVYCCRVHRGWENDMKITV	120
Qy	121	SLEIVPPKVTTPDIVTTVPVTTVTRSTTVPT-----TTTVPVTTTVPVTTTMSIPTTTTVP	174
Db	121	SLGIVPPKVTTPDIVTTVPVTTVTRSTTVPTTTTVPMTTTPVTTTVPVTTTMSIPTTTTVP	180
Qy	175	TTMTVSTTTSVPVTTTSIPTTTTSVPVTTVSTFVPPMPLPRQNHVPVATSPSSQPPAETHP	234
Db	181	TTMTVSTTTSVPVTTTSIP-TTISVPVTTVSTFVPPMPLPRQNHVPVATSPSSQPPAETHP	239
Qy	235	TTLOGAIRREPTSSPLYSVTTDGNDTVTESSDGLWNNNOTQLEHSLLTANTTKGIYAG	294
Db	240	TTLOGAIRREPTSSPLYSVTTDGDVTVTESSDGLWNNNOTQLEHSLLTANTTKGIYAG	299
Qy	295	VCISVLVLLALLGVIIAKKYFFKKEVQQL	323
Db	300	VCISVLVLLALLGVIIAKKYFFKKEVQQL	328

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Job time : 238.54 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 08:57:16 ; Search time 133.862 Seconds
(without alignments)
1277.688 Million cell updates/sec

Title: US-10-718-321-7
Perfect score: 1749
Sequence: 1 MHPQVILSLILHLADSVAG.....FPKKEVQQLRPHKSCIHORE 334

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03:.*
1: uniprot_eprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1684	96.3	359	2	O43656 homo sapien
2	1661.5	95.0	364	2	Q96D42
3	1309	74.8	451	2	Q95144
4	1303.5	74.5	460	2	O18984
5	1288	73.6	469	2	O7J348
6	1288	73.6	474	2	O46597
7	1286	73.5	473	2	O7JJ47
8	1286	73.5	478	2	O46598
9	522.5	29.9	307	2	O54947
10	519	29.7	305	2	O8VIM2
11	491.5	28.1	282	2	O8VIM1
12	486.5	27.8	282	2	O7TFU2
13	401	22.9	305	2	O8VIM0
14	401	22.9	362	2	O8CIC7
15	399	22.8	343	2	O6U7R3
16	398	22.8	343	2	O6U7R4
17	392	22.4	305	2	O8R183
18	385	22.0	438	2	Q6INH8
19	367.5	21.0	378	2	O96H15
20	283	16.2	281	2	O8VIM0
21	269	15.4	192	2	O7TQ03
22	267	15.3	301	2	O96K94
23	266	15.2	301	2	O8TDQ0
24	254	14.5	224	2	O6G6V2
25	250	14.3	582	2	O8IR74
26	246.5	14.1	662	1	MUC1_XENLA
27	246	14.1	538	2	O76H84
28	244	14.0	400	1	MUA1_XENLA
29	238	13.6	483	2	O9W4M2
30	235.5	13.5	142	2	O8WW60
31	235.5	13.5	468	2	O55279

RESULT 1

O43656		PRELIMINARY;		PRT; 359 AA.	
ID	O43656				
AC	O43656;				
DT	01-JUN-1998	(TrEMBLrel. 06, Created)			
DT	01-JUN-1998	(TrEMBLrel. 06, Last sequence update)			
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)			
DE	Hepatitis A virus cellular receptor 1.				
GN	Name=hHAVcr-1;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Liver;				
RA	MEDLINE=98325180; PubMed=9658108;				
RA	Feigelsstock D., Thompson P., Mattoo P., Zhang Y., Kaplan G.G.;				
RT	"The human homolog of HAVcr-1 codes for a hepatitis A virus cellular receptor.";				
RL	J. Virol. 72:6621-6628(1998).				
DR	EMBL	AF043724	RAC39862.1	-	
DR	GO	GO:0004872	Fireceptor activity	IEA.	
DR	InterPro	IPR003599	IG.		
DR	InterPro	IPR007110	IG-like.		
DR	InterPro	IPR003006	IG_MHC.		
DR	SMART	SM00409	IG_1.		
DR	PROSITE	PS50835	IG_LIKE; 1.		
DR	PROSITE	PS00290	IG_MHC; UNKNOWN_1.		
KW	Receptor.				
SEQ	SEQUENCE 359 AA; 38704 MW; C207FEC562DC62CA CRC64;				
Query Match 96.3%; Score 1684; DB 2; Length 359;					
Best Local Similarity 100.0%; Pred. No.5.le-101;					
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	MHPQVILSLILHLADSVAGSVKVGGEAGPSVTLPCHYSGAVTSMCNRGSCSLFTCQNG	60		
DB	1	MHPQVILSLILHLADSVAGSVKVGGEAGPSVTLPCHYSGAVTSMCNRGSCSLFTCQNG	60		
QY	61	IWTNGTHVTRKDYRKLGLDLSRDDVSLTIENTAVSDSGVCCVHRGFNFMKITY	120		
DB	61	IWTNGTHVTRKDYRKLGLDLSRDDVSLTIENTAVSDSGVCCVHRGFNFMKITY	120		
QY	121	SLEIIPPVKVTTPIVTTVPTVTVTSTVPTTTVPTTTVPTTTVPTTTVPTT	180		
DB	121	SLEIIPPVKVTTPIVTTVPTVTVTSTVPTTTVPTTTVPTTTVPTTTVPTT	180		
QY	181	TTTSVPTTTSIPTTTSVPTTTSVPTTTSVPTTTSVPTTTSVPTTTSVPTT	240		
DB	181	TTTSVPTTTSIPTTTSVPTTTSVPTTTSVPTTTSVPTTTSVPTTTSVPTT	240		
QY	241	IRREPTSSPLSYTTDGDNDVTTESSDGLNWNQTLFLEHSLLTANTTGGIYAGVCISVL	300		

ALIGNMENTS

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Db      241  IRREPTSSPLSYTTDGNDDTVTSSDGLWNNNOTQLFLEHSLLTANTTKGIYAGVCISVL 300
QY      301  VLLALLGVIIAKKYFFKKEVQQL 323
Db      301  VLLALLGVIIAKKYFFKKEVQQL 323

RESULT 2
Q96D42  ID Q96D42      PRELIMINARY;      PRT;      364 AA.
AC      Q96D42;
DT      01-DEC-2001 (TRENBLrel. 19, Created)
DT      01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT      25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE      HAVCR1 protein.
GN      Name=HAVCR1;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Kidney;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA      Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA      Jones S.J., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Kidney;
RA      Strausberg R.;
RA      Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RA      Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RA      Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BC013325; AAH13325.1; -.
DR      EMBL; CR457114; CAG33395.1; -.
DR      Genew; HGNC:17866; HAVCR1.
DR      InterPro; IPR003599; IG.
DR      InterPro; IPR007110; IG-like.
DR      InterPro; IPR003006; IG_MHC.
DR      SMART; SM00409; IG; 1.
DR      PROSITE; PS50835; IG LIKE; 1.
DR      PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ      SEQUENCE 364 AA; 39249 MW; AA67C7DC7FAC81F1 CRC64;

Query Match      95.0%; Score 1661.5; DB 2; Length 364;
Best Local Similarity 98.2%; Pred. No. 1.5e-99;
Matches 322; Conservative 0; Mismatches 1; Indels 5; Gaps 1;

QY      1  MHPQVILSLIHLADSVAGSVKVGGEAGPSVTLPCHYSGAVTSCMWRGSCSLFTCCNG 60
Db      1  MHPQVILSLIHLADSVAGSVKVGGEAGPSVTLPCHYSGAVTSCMWRGSCSLFTCCNG 60
QY      61  IVWTNGTHVTKRYKLLGDLSDRDVSLTIENTAVSDSGVYCCRVHRGFNFMKITY 120

RESULT 3
Q95144  ID Q95144      PRELIMINARY;      PRT;      451 AA.
AC      Q95144;
DT      01-FEB-1997 (TRENBLrel. 02, Created)
DT      01-FEB-1997 (TRENBLrel. 02, Last sequence update)
DT      01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE      HAVcr-1 protein precursor.
OS      Cercopithecus aethiops (Green monkey) (Grivet).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC      Cercopithecinae; Cercopithecus.
OX      NCBI_TaxID=9534;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Kidney;
RA      MEDLINE=97015129; PubMed=8861957;
RA      Kaplan G., Totsuka A., Thompson P., Akatsuka T., Moritsugu Y.,
RA      Feinstein S.M.;
RA      "Identification of a surface glycoprotein on African green monkey
RA      kidney cells as a receptor for hepatitis A virus.";
RL      EMBO J. 15:4282-4296(1996).
DR      EMBL; X98252; CAA66906.1; -.
DR      PIR; S71754; S71754.
DR      InterPro; IPR003599; IG.
DR      InterPro; IPR007110; IG-like.
DR      InterPro; IPR003006; IG_MHC.
DR      SMART; SM00409; IG; 1.
DR      PROSITE; PS50835; IG LIKE; 1.
DR      PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW      Signal.
FT      SIGNAL.
SQ      SEQUENCE 451 AA; 48774 MW; 5D395C5455AA4332 CRC64;

Query Match      74.8%; Score 1309; DB 2; Length 451;
Best Local Similarity 63.3%; Pred. No. 1e-76;
Matches 255; Conservative 36; Mismatches 32; Indels 80; Gaps 3;

QY      1  MHPQVILSLIHLADSVAGSVKVGGEAGPSVTLPCHYSGAVTSCMWRGSCSLFTCCNG 60
Db      1  MHPQVILSLIHLADSVAGSVKVGGEAGPSVTLPCRYNGAITSICMWRGTCVFCSCPFG 60
QY      61  IVWTNGTHVTKRYKLLGDLSDRDVSLTIENTAVSDSGVYCCRVHRGFNFMKITY 120
Db      61  IVWTNGTHVTKRYKLLGDLSDRDVSLTIENTAVSDSGVYCCRVHRGFNFMKITY 120
QY      121  SLEIVPPKV-----TTTIVTTP-----TTTIVTTP 139
Db      121  SLKIGPPRVTPIVRTVTSVTPVTTTLPVTTTLPVTTTLPVTTTLPVTTTLP 180
QY      140  TTTVTSSTVPTTTP-----TTTPTTMSIPTTTTPTTPTT 182
Db      181  TTTVPTTTPVTTTTPVTTTTPVTTTTPVTTTTPVTTTTPVTTTTPVTTTTP 240

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Db      61  IVWTNGTHVTKRYKLLGDLSDRDVSLTIENTAVSDSGVYCCRVHRGFNFMKITY 120
QY      121  SLEIVPPKVTTTTPVTTTTPVTTTTPVTTTTPVTTTTPVTTTTPVTTTTPVTTTTP 175
Db      121  SLEIVPPKVTTTTPVTTTTPVTTTTPVTTTTPVTTTTPVTTTTPVTTTTPVTTTTP 180
QY      176  TMTVSTTTSVPTTTSIPTTTSVPVTTTTSVTPVPPMLPRQNHPEVATSPSSQPAETHPT 235
Db      181  TMTVSTTTSVPTTTSIPTTTSVPVTTTTSVTPVPPMLPRQNHPEVATSPSSQPAETHPT 240
QY      236  TLQGAIRREPTSSPLSYTTDGNDDTVTSSDGLWNNNOTQLFLEHSLLTANTTKGIYAGV 295
Db      241  TLQGAIRREPTSSPLSYTTDGNDDTVTSSDGLWNNNOTQLFLEHSLLTANTTKGIYAGV 300
QY      296  CISVLVLLALLGVIIAKKYFFKKEVQQL 323
Db      301  CISVLVLLALLGVIIAKKYFFKKEVQQL 328

RESULT 3
Q95144  ID Q95144      PRELIMINARY;      PRT;      451 AA.
AC      Q95144;
DT      01-FEB-1997 (TRENBLrel. 02, Created)
DT      01-FEB-1997 (TRENBLrel. 02, Last sequence update)
DT      01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE      HAVcr-1 protein precursor.
OS      Cercopithecus aethiops (Green monkey) (Grivet).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC      Cercopithecinae; Cercopithecus.
OX      NCBI_TaxID=9534;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Kidney;
RA      MEDLINE=97015129; PubMed=8861957;
RA      Kaplan G., Totsuka A., Thompson P., Akatsuka T., Moritsugu Y.,
RA      Feinstein S.M.;
RA      "Identification of a surface glycoprotein on African green monkey
RA      kidney cells as a receptor for hepatitis A virus.";
RL      EMBO J. 15:4282-4296(1996).
DR      EMBL; X98252; CAA66906.1; -.
DR      PIR; S71754; S71754.
DR      InterPro; IPR003599; IG.
DR      InterPro; IPR007110; IG-like.
DR      InterPro; IPR003006; IG_MHC.
DR      SMART; SM00409; IG; 1.
DR      PROSITE; PS50835; IG LIKE; 1.
DR      PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW      Signal.
FT      SIGNAL.
SQ      SEQUENCE 451 AA; 48774 MW; 5D395C5455AA4332 CRC64;

Query Match      74.8%; Score 1309; DB 2; Length 451;
Best Local Similarity 63.3%; Pred. No. 1e-76;
Matches 255; Conservative 36; Mismatches 32; Indels 80; Gaps 3;

QY      1  MHPQVILSLIHLADSVAGSVKVGGEAGPSVTLPCHYSGAVTSCMWRGSCSLFTCCNG 60
Db      1  MHPQVILSLIHLADSVAGSVKVGGEAGPSVTLPCRYNGAITSICMWRGTCVFCSCPFG 60
QY      61  IVWTNGTHVTKRYKLLGDLSDRDVSLTIENTAVSDSGVYCCRVHRGFNFMKITY 120
Db      61  IVWTNGTHVTKRYKLLGDLSDRDVSLTIENTAVSDSGVYCCRVHRGFNFMKITY 120
QY      121  SLEIVPPKV-----TTTIVTTP-----TTTIVTTP 139
Db      121  SLKIGPPRVTPIVRTVTSVTPVTTTLPVTTTLPVTTTLPVTTTLPVTTTLP 180
QY      140  TTTVTSSTVPTTTP-----TTTPTTMSIPTTTTPTTPTT 182
Db      181  TTTVPTTTPVTTTTPVTTTTPVTTTTPVTTTTPVTTTTPVTTTTPVTTTTP 240

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RESULT 6
O46597 PRELIMINARY; PRT; 474 AA.
ID Q7JJ47
AC Q7JJ47
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-1998 (TREMBlrel. 26, Last annotation update)
DE Hepatitis A virus cellular receptor 1 long form.
GN Name=HAVcr-1;
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98285791; PubMed=9621093;
RA Feigelshtock D., Thompson P., Mattoo P., Kaplan G.G.;
RT "Polymorphisms of the hepatitis A virus cellular receptor 1 in African
RT green monkey kidney cells result in antigenic variants that do not
RT react with protective monoclonal antibody 190/4.";
RL J. Virol. 72:6218-6222(1998).
DR EMBL; AF043447; AAC39772.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG_1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 474 AA; 51088 MW; 472DF987CA220524 CRC64;

Query Match 73.6%; Score 1288; DB 2; Length 474;
Best Local Similarity 59.9%; Pred. No. 2.5e-75;
Matches 252; Conservative 39; Mismatches 32; Indels 98; Gaps 3;

QY 1 MHPQVILSLIHLADSVAGSVKVGEGAPSVTLPCYSGAVTSCMNRGCSLFTCONG 60
DB 6 MHLQVILSLIHLADSVAGSVKVGEGAPSVTLPCYSGAVTSCMNRGCSLFTCONG 65
QY 61 IWTNGTHVTYRKDTRYKLLGDLRRDVSLLTAVSDSGVYCCRVHRGFNDMKITV 120
DB 66 IWTNGTHVTYRKDTRYKLLGDLRRDVSLLTAVSDSGVYCCRVHRGFNDMKITI 125
QY 121 SLEIVPPKV----- 130
DB 126 SLKIGPPRVTPIVRTVTSSTVPTTTTTLPTTTTLPTTTTLPTTTTLPTTTTLPTTT 185
QY 131 -----TTPIVTPVTVTVTS 147
DB 186 LPTTTTVPMTTTLPTTLPTTTTLPTTLPTTTTLPTTLPTTTTLPTTTTLPTTTTLPTTT 245
QY 148 TTVPTTTTVP-TTIVPT---TMSIPTTTTVPMTVSTVPTTTSIPTTTSVPVTT 202
DB 246 TLPPTTTTTLPTTLPTTLPTTLPTTLPTTLPTTLPTTLPTTLPTTLPTTLPTTLPTTT 305
QY 203 VSTFVPMPPLPQNHEPVATSPSSQPAETHPTTLQGAIRREPTSSPLSYTTDGNVT 262
DB 306 VSTFVPPTPLPQDHEPVATSPSSQPAETHPTVLLGATRTQPTSSPLSYTTDGSIVT 365
QY 263 ESSDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVLVLLALLGVIAKKYFFKVEQQ 322
DB 366 ESSDGLWNNQTLSPHSQPMVNTTEGIYAGVCISVLVLLAVLGVIAKKYFFKBIQQ 425
QY 323 L 323
DB 426 L 426

RESULT 7
O46598 PRELIMINARY; PRT; 478 AA.
ID Q46598
AC O46598
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DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hepatitis A virus cellular receptor 1 long form.
GN Name=HAVcr-1;
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98285791; PubMed=9621093;
RA Feigelscock D., Thompson P., Mattoo P., Kaplan G.G.;
RT "Polymorphisms of the hepatitis A virus cellular receptor 1 in African
RT green monkey kidney cells result in antigenic variants that do not
RT react with protective monoclonal antibody 190/4.";
RL J. Virol. 72:6218-6222(1998).
DR EMBL; AF043449; AAC39774.1; -
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00409; IG_1.
DR PROSITE; PS50835; IG-LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 478 AA; 51501 MW; 3A919655C752FF60 CRC64;
Query Match 73.5%; Score 1286; DB 2; Length 478;
Best Local Similarity 58.9%; Pred. No. 3.4e-75;
Matches 251; Conservative 38; Mismatches 33; Indels 104; Gaps 2;
QY 1 MHPQVILSLHLADSVAGSVKVGEGAPSVTLPCYSGAVTSMCWNRGSCSLFTCONG 60
DB 6 MHPQVILSLHLADSVAGSVKVGEGAPSVTLPCYSGAVTSMCWNRGSCSLFTCONG 65
QY 61 IVWNGTHVYRKDTRYKLLGDLSSRDVSLTIENAVSDSGVYCCVRHGFNDFMKITV 120
DB 66 IVWNGTHVYRKDTRYKLLGDLSSRDVSLTIENAVSDSGVYCCVRHGFNDFMKITV 125
QY 121 SLEIVPPKV----- 129
DB 126 SLKIGPRVTPPIVTRVTRSTTVPTTTTTLPTTTTLPTTTTLPTTTTLPTMTT 185
QY 130 -----TTTPIVTT 137
DB 186 LPTTTVPMTTLPTTLPTTTTLPTTLPTTTTLPTTLPTTTTLPTTLPTMTTLP 245
QY 138 VPTTVTRSTTVPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTTT 197
DB 246 LPTTTTLPTTTTLPTTTTLPTTLPTTLPTTLPTTLPTTLPTTTTLPTTTTL 304
QY 198 PTTTVSTVTPWMLPRQHHEPVATSPSPQAEHTPTTLOGAIRREPTSSPLSYT 257
DB 305 PTTTWSTVTPPTLPMQDHEPVATSPSPQAEHTPTTLOGAIRREPTSSPLSYT 364
QY 258 NDTVTSSDGLWNNNTQLFLHSLLTANTTKIGYAGVCISLVLLALLGVIAKRY 317
DB 365 SDTVTSSDGLWNNNTQLSPHSPQWNTTEGIYAGVCISLVLLALLGVIAKRY 424
QY 318 KEVQQL 323
DB 425 KEIQQL 430
RESULT 9
ID O54947 PRELIMINARY; PRT; 307 AA.
AC O54947;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Kidney injury molecule-1 (KIM-1 protein).
GN Name=KIM-1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley; TISSUE=Kidney;
RX MEDLINE=98129827; PubMed=9461608; DOI=10.1074/jbc.273.7.4135;
RA Ichimura T., Bonventre J.V., Bailly V., Wei H., Hession C.A.,
RA Cate R.L., Sanicola M.;
RT "Kidney injury molecule-1 (KIM-1), a putative epithelial cell adhesion
RT molecule containing a novel immunoglobulin domain, is up-regulated in
RT renal cells after injury.";
RL J. Biol. Chem. 273:4135-4142(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF035963; AAC53546.1; -
DR EMBL; BC061820; AH61820.1; -
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00409; IG_1.
DR PROSITE; PS50835; IG-LIKE; 1.
SQ SEQUENCE 307 AA; 33963 MW; 736D1DD1F1549760 CRC64;
Query Match 29.9%; Score 522.5; DB 2; Length 307;
Best Local Similarity 39.4%; Pred. No. 4.2e-26;
Matches 128; Conservative 39; Mismatches 93; Indels 65; Gaps 12;
QY 4 QVVLISLHLHLADSVAGSVKVGEGAPSVTLPCYSGAVTSMCWNRGSCSLFTCONGI 61
DB 5 QVFLISLHLHLADSVAGSVKVGEGAPSVTLPCYSGAVTSMCWNRGSCSLFTCONGI 64
QY 62 VWTNGTHVYRKDTRYKLLGDLSSRDVSLTIENAVSDSGVYCCVRHGFNDFMKITV 121
DB 65 IWTNGVQVYRSGRYNIGRISGDDVSLTIENAVSDSGVYCCVRHGFNDFMKITV 124
QY 122 LEIVPPKVTTPIVTTVPVTTVTRSTTVPTT-----TTTVPVTTVPTTMSIPTTTVPTMTV 179
DB 125 LE-VKPEIPTSP-----PTRPTTRPTTRPTTIS----- 153
QY 180 STTTSVPVTTTSTPTTTSVPVTTTSTVFPVPPMLPRQHHEPVATSPSPQAEHTPTTLOG 239
DB 154 TRSTHVTPTSTVSTST-----PTPEQQTQTHKPEITT-----FYAHETT--- 191
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QY 240 AIRREPTSSPLYSTYTDGNDVTSSDGLNWNQTLFLEHSLLTANTTKGIYAGVCISV 299
DB 192 ---AEVTETPSY-T-PADWNGT-VT-SSSEAWNNHTVRIPLRPK-QRNPTKGFYVGMSVAA 244
QY 300 LVLLALLGVIIAKKY-FPKKVEVOQL 323
DB 245 LLLLLLASTVVVTVRIIRKKMGL 269

RESULT 10
Q8VIM2 PRELIMINARY; PRT; 305 AA.
AC Q8VIM2;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE TIM1.
GN Name=Havcr1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/c; TISSUE=Spleen;
RX MEDLINE=21582130; PubMed=11725301;
RA McIntire J.J., Umetsu S.E., Akbari O., Potter M., Kuchroo V.K.,
RA Barsh G.S., Freeman G.J., Umetsu D.T., DeKruyff R.H.;
RT "Identification of Tapr (an airway hyperreactivity regulatory locus)
and the linked rim gene family.";
RL Nat. Immunol. 2:1109-1116(2001).
DR EMBL; AF399829; AAL35774.1; -.
DR MGD; MGI:2159680; Havcr1.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR SMART; SM00409; IG, 1.
DR PROSITE; PS50835; IG LIKE, 1.
SQ SEQUENCE 305 AA; 33391 MW; 8F4EA38627FE85FB CRC64;

Query Match 29.7%; Score 519; DB 2; Length 305;
Best Local Similarity 40.6%; Pred. No. 7e-26;
Matches 129; Conservative 34; Mismatches 95; Indels 60; Gaps 12;

QY 4 QVILSLILHLADSVAGSVKVGEGAPSVTLPCCHYS--GAVTSMCMNRGSCSLFTQNGI 61
DB 5 QVFISGLILLPGTVDVSVEKGVGVHPVTLPCYTVSTYRGITTCWGRGQCPSSACQNTL 64
QY 62 VWTNGTHVYRKDTRYKLLGDLRRDVSILTIENTAVSDGVYCCRVHRGWFNDMKITVS 121
DB 65 IWTNGHRVYQKSSRYNLKGHISEGDSVLSITIENSVEDSGLYCCRVHPGWFNDQKVTFS 124
QY 122 LEIVPPKVTTPPIVTVPTVTVTRSTTVPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 181
DB 125 LQVKP-----EIPTRPPTTRPTATGRPT-----ISTRSTHVPTTSIRVS 167
QY 161 TTTSVPTTTSIPTTTSVPVTTTSTVTFVPMPLPRQNHPEVATSPSSQPAPETHPTTLOGA 240
DB 168 TSTP-PTSTH--TWTHKEPPI---TFCP-----HETAE-- 195
QY 241 IRREPTSSPLYSTYTDGNDVTSSDGLNWNQTLFLEHSLLTANTTKGIYAGVCISVL 300
DB 196 VTGIFSHPT----TDWNGTVTSSGD-TWSNHTEA--IPPGKPKQNPTKGFYVGICIAAL 247
QY 301 VLLALLGVIIAKKYFPKK 318
DB 248 LLLLLVSTVAITRYILMK 265

RESULT 11
Q8VIM1 PRELIMINARY; PRT; 282 AA.
AC Q8VIM1;
DT 01-MAR-2002 (TREMBlrel. 20, Created)

```

```

DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE TIM1.
GN Name=Havcr1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2; TISSUE=Spleen;
RX MEDLINE=21582130; PubMed=11725301;
RA McIntire J.J., Umetsu S.E., Akbari O., Potter M., Kuchroo V.K.,
RA Barsh G.S., Freeman G.J., Umetsu D.T., DeKruyff R.H.;
RT "Identification of Tapr (an airway hyperreactivity regulatory locus)
and the linked rim gene family.";
RL Nat. Immunol. 2:1109-1116(2001).
DR EMBL; AF399830; AAL35775.1; -.
DR MGD; MGI:2159680; Havcr1.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR SMART; SM00409; IG, 1.
DR PROSITE; PS50835; IG LIKE, 1.
SQ SEQUENCE 282 AA; 30968 MW; 7D30BE0698F0AC5F CRC64;

Query Match 28.1%; Score 491.5; DB 2; Length 282;
Best Local Similarity 36.6%; Pred. No. 3.9e-24;
Matches 116; Conservative 32; Mismatches 88; Indels 81; Gaps 7;

QY 4 QVILSLILHLADSVAGSVKVGEGAPSVTLPCCHYS--GAVTSMCMNRGSCSLFTQNGI 61
DB 5 QVFISGLILLPGAVDSVVEKGVGVHPVTLPCYTVSTYRGITTCWGRGQCPSSACQNTL 64
QY 62 VWTNGTHVYRKDTRYKLLGDLRRDVSILTIENTAVSDGVYCCRVHRGWFNDMKITVS 121
DB 65 IWTNGHRVYQKSSRYNLKGHISEGDSVLSITIENSVEDSGLYCCRVHPGWFNDQKVTFS 124
QY 122 LEIVPPKVTTPPIVTVPTVTVTRSTTVPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 181
DB 125 LQVKP-----EIPTRPPTTRPTATGRPT-----TIST 155
QY 182 TTTSVPTTTSIPTTTSVPVTTTSTVTFVPMPLPRQNHPEVATSPSSQPAPETHPTTLOGAI 241
DB 156 -----RSTHVPTSTRVSTP----- 171
QY 242 RREPTSSPLYSTYTDGNDVTSSDGLNWNQTLFLEHSLLTANTTKGIYAGVCISVLV 301
DB 172 ---PTSTHTWTHKPDWNGTVTSSGD-TWSNHTEA--IPPGKPKQNPTKGFYVGICIAALL 225
QY 302 LLALLGVIIAKKYFPKK 318
DB 226 LLLLVSTVAITRYILMK 242

RESULT 12
Q7TPU2 PRELIMINARY; PRT; 282 AA.
AC Q7TPU2;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Blastocyst;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J.C., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smaluk J., Schermer A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2].
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Blastocyst;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053400; AAH53400.1; -;
DR InterPro; IPR003599; IG-like.
DR SMART; IPR007110; IG-like.
DR PROSITE; PS00409; IG; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Hypothetical protein.
SQ SEQUENCE 282 AA; 30938 MW; 6D31E2778480AC5F CRC64;

Query Match 27.8%; Score 486.5; DB 2; Length 282;
Best Local Similarity 36.3%; Pred. No. 8.1e-24;
Matches 115; Conservative 32; Mismatches 89; Indels 81; Gaps 7;

QY 4 QVILSLILHLADSVAGSVKVGEGAPSVTLPCYHS--GAVTSMCNWRCGSLFTQCGI 61
DB 5 QVFISGLILLLPGAVDSYVEVGVGHPVTLCTYTRGRTTTCWGRGQCPSSACQNTL 64

QY 62 VWTNGTHVTRKDYKLLGLDLSRRDVSLLTIENTAVSDSGVCCRVHRGWFNDMKITVS 121
DB 65 IWTNGHRTVYKSRYNLKGHISEGVSLLTIENTAVSDSGVCCRVHRGWFNDQKVTFS 124

QY 122 LEIVPPKVTTPITVPTVTRSTVPTVTTTPTVTTTPTVTTTPTVTTTPTVTTTPTVTT 181
DB 125 LQVKP-----EIPTRPPRRPTTTPATGRPT-----AIST 155

QY 182 TTSVPTTTSIPTTSVPTTSTVTFVPPMPLRQNHPEVATSPSSPPQPAETHPTTLOGAI 241
DB 156 -----RSTHVPTSTRVSTSTP----- 171

QY 242 RREPTSSPLSYTTDGNVTSTSSDGLWNNNTQFLFLEHSLLTANTTKGIYAGVCISVLV 301
DB 172 ----PTSTHTWTHKPDWNGVTSSGD--TWSNHTEA--IPPKQPKQKPTKGVYGCIAL 225

QY 302 LLALLGVIIAKKYFFKK 318
DB 226 LLLLVSTVAITRYILMK 242

RESULT 13
Q8VBWO PRELIMINARY; PRT; 305 AA.
AC Q8VBWO;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Name=Timd2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2, and BALB/c; TISSUE=Spleen;
RX MEDLINE=21582130; PubMed=11725301;
RA McIntire J.J., Umetsu S.E., Akbari O., Potter M., Kuchroo V.K.,
RA Barah G.S., Freeman G.J., Umetsu D.T., Dekruyff R.H.;
RT "Identification of Tapr (an airway hyperreactivity regulatory locus)
RT and the linked Tim gene family.";
RL Nat. Immunol. 2:1109-1116(2001).
DR EMBL; AF399828; AAL35773.1; -;
DR EMBL; AF399827; AAL35772.1; -;
DR MGD; MGI:2159681; Timd2.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS0835; IG LIKE; 1.
SQ SEQUENCE 305 AA; 33519 MW; 68B69370FE23C9D0 CRC64;

Query Match 22.9%; Score 401; DB 2; Length 305;
Best Local Similarity 33.5%; Pred. No. 2.9e-18;
Matches 108; Conservative 48; Mismatches 92; Indels 74; Gaps 12;

QY 4 QVILSLILHLADSVAGSVKVGEGAPSVTLPCYHS--GAVTSMCNWRCGSLFTQCGI 60
DB 5 QVFISGLILLLPGAVESHTAVOGLAGHPVTLPCISTHGLGIVPMCWGEGECHRSHYCS 64

QY 61 IYWTNGTHVTRKDYKLLGLDLSRRDVSLLTIENTAVSDSGVCCRVHRGWFNDMKITV 120
DB 65 LIWTNGYTVTHQRNSRYQLKGNISGVSLLTIENTAVSDSGVCCRVHRGWFNDQKVTFS 122

QY 121 SLIEIVPPKVTTPITVPTVTRSTVPTVTTTPTVTTTPTVTTTPTVTTTPTVTTTPTV 180
DB 123 MLE-VKPEISTSTP-----PTR-----PTATGRPTTIS-T 149

QY 181 TTSVPTTTSIPTTSVPTTSTVTFVPPMPLRQNHPEVATSPSSPPQPAETHPTT 236
DB 150 RSTHVPTSTRVSTSTP-----PTAHTETIKPEATTFPDQTAETVELPST 197

QY 237 LQGAIRREPTSSPLSYTTDGNVTSTSSDGLWNNNTQFLFLEHSLLTANTTKGIYAGVC 296
DB 198 -----PADWENTVT--SSDDPDWDDN--TEV--IPPKQPKQKLNKGFVVGIS 237

QY 297 ISVLVLLALLGVIIAKKYFFKK 318
DB 238 IAALLILMLLSTMTVITRYVVMK 259

RESULT 14
Q8CIC7 PRELIMINARY; PRT; 362 AA.
AC Q8CIC7;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE T-cell immunoglobulin and mucin domain containing 4.
GN Name=Timd4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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OM protein - protein search, using sw model

Run on: . June 29, 2005, 08:57:16 ; Search time 3.79568 Seconds
(without alignments)
1064.659 Million cell updates

Title: US-10-718-321-6 COPY 40 81

Perfect score: 225
Sequence: 1 PLYSYTTCGNDTIVTESDGL.....NNQTQFLFLEHSLTANTTKG 42

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processed virgin. Virgin. Vol. 1. 98

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:★

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1:  p1r1:*
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2: pir2: *

```
3: pir3:*
4: pir4:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	178	79.1	451	2	S71754	cellular hepatitis	
2	62.5	27.8	639	2	S49559	mitochondrial outer	
3	61.5	27.3	1289	2	A90367	proteinase related	
4	60	26.7	602	2	A45769	acetylcholine rece	
5	59	26.2	1254	1	JQ1978	structural polypro	
6	58	25.8	1254	1	VHWVVE	structural polypro	
7	58	25.8	1254	1	VHWVVT	structural polypro	
8	58	25.8	1255	1	B44213	structural polypro	
9	58	25.8	1255	1	D44213	structural polypro	
10	57.5	25.6	405	2	H89330	protein R11G1.14	
11	57	25.3	2399	2	V18799	toxin-like outer m	
12	56.5	25.1	326	1	VGXREER	glycoprotein VP7 p	
13	56.5	25.1	338	2	S75217	N-acetyl-muramoyl-L	
14	56.5	25.1	1658	2	D86890	DNA-directed DNA p	
15	56	24.9	472	2	S36519	L2 protein - human	
16	55.5	24.7	322	2	T23891	hypothetical prote	
17	55	24.4	826	1	T02753	S-receptor kinase	
18	55	24.4	846	2	C82135	chitinase VC1952 [
19	54.5	24.2	189	2	B26659	T-cell receptor ga	
20	54.5	24.2	205	2	B26425	T-cell receptor ga	
21	54.5	24.2	213	2	T01715	hypothetical prote	
22	54.5	24.2	285	2	G85016	probable myb-relat	
23	54.5	24.2	304	2	S04663	T-cell receptor ga	
24	54.5	24.2	323	2	S01895	T-cell receptor ga	
25	54.5	24.2	386	2	A82284	conserved hypothet	
26	54.5	24.2	639	2	A55019	muscarinic acetylch	
27	54.5	24.2	923	2	E70820	hypothetical glycol	
28	54	24.0	735	2	B83763	catalase BH0906 [i	
29	54	24.0	891	2	T30812	ubiquitin-protein	

30	54	24.0	2013	2	C71610	probable membrane
31	54	24.0	2018	2	T34274	hypothetical prote
32	53.5	23.8	189	2	A69479	conserved hypothet
33	53.5	23.8	760	2	S64023	ALK1 protein - yea
34	53.5	23.8	1254	1	JQ1979	structural polypro
35	53	23.6	80	1	ASLJBY	ori-Y protein - bo
36	53	23.6	245	2	E86450	F5D14.29 protein -
37	53	23.6	321	2	T45053	hypothetical prote
38	53	23.6	350	2	I38403	neu differentiatio
39	53	23.6	394	2	T18752	hypothetical prote
40	53	23.6	462	2	I38404	neu differentiatio
41	53	23.6	576	2	T38666	probable tri-p asp r
42	53	23.6	637	2	C43273	hergulin precursor
43	53	23.6	640	2	C43273	hergulin precursor
44	53	23.6	645	2	B43273	hergulin, splice
45	53	23.6	652	2	T39409	hypothetical prote

ALIGNMENTS

RESULT 1
S71754 cellular hepatitis A receptor HAVcr-1 precursor - green monkey
N:Alternate names: surface glycoprotein
C:Species: Cercopithecus aethiops (green monkey, grivet)
C:Date: 29-Jan-1998 #sequence_revision 06-feb-1998 #text_change 09-Jul-2004
C:Accession: S71754
R:Kaplan, G.; Totsuka, A.; Thompson, P.; Akatsuka, T.; Moritsugu, Y.; Feinstein
EMBO J. 15, 4282-4296, 1996
A:Title: Identification of a surface glycoprotein on African green monkey kidney
A:Reference number: S71754; MUID:97015129; PMID:8961957
A:Accession: S71754
A:Molecule type: mRNA
A:Residues: 1-451 <YAP>
A:Cross-references: UNIPROT:Q95144; EMBL:X98252; NID:gl526573; PID:e247449; PID
A:Experimental source: kidney
C:Keywords: glycoprotein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-451/Product: cellular hepatitis A receptor HAVcr-1 #status predicted <MAT>

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Query Match          79.1%; Score 178; DB 2; Length 451;
Best Local Similarity 81.0%; Pred. No. 1.7e-14;
Matches 34: Conservative 2; Mismatches 6; Indels 0; Gaps 0;

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QY 1 PLYSTTDGNDVTVESSDGLWNNQTLFLEHSLLTANTTKG 42
|||||:||||| ||| |||:
pb 329 PLYSTTDGSDVTVESSDGLWNNQTLSPHSPOMNTTEG 370

RESULT 2

S48959
mitochondrial outer membrane protein TOM71 - Yeast (*Saccharomyces cerevisiae*)
S48959
A/Alternate names: protein Yhr117w
C/Species: *Saccharomyces cerevisiae*
C/Date: 13-Jan-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
C/Accession: S48959; S62886
R/Jatzeille, F.
submitted to the EMBL Data Library, May 1994
A/Description: The sequence of *S. cerevisiae* cosmid 8263.
A/Reference number: S46676
A/Accession: S48959
A/Molecule type: DNA
A/Residues: 1-639 <LAT>
A/Cross references: UNIPROT:P38825; EMBL:U00059; NID:G529116; PIDN:AAB68868.1
R/Boemer, U.; Pfanner, N.; Dietmeier, K.
FEBS Lett. 382, 153-158, 1996
A/Title: Identification of a third yeast mitochondrial Tom protein with tetra
A/Reference number: S62886; MUID:96196584; PMID:8612740
A/Accession: S62886
A/Status: nucleic acid sequence not shown; not compared with conceptual trans
A/Molecule type: DNA
A/Residues: 1-639 <BOE>


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F:1231-1247/Domain: transmembrane #status predicted <TM4>
F:47,286,546,625,652,946/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match      25.8%; Score 58; DB 1; Length 1254;
Best Local Similarity 47.6%; Pred. No. 54;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 11 DVTWSSDGLWNNNQTLFLE 31
      : ||| |||||
Db 758 ETTWESLDHLWNNNQMFQ 778
      : ||| |||||

RESULT 7
VHWVVT
structural polyprotein - Venezuelan equine encephalitis virus (strain TRD)
N:Contains: 6K protein; coat protein; membrane glycoprotein E1; membrane glycoprotein E2
C:Species: Venezuelan equine encephalitis virus
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: B31467; A47612
R:Kinney, R.M.; Johnson, B.J.B.; Welch, J.B.; Teuchiya, K.R.; Trent, D.W.
Virology 170, 19-30, 1989
A:Title: The full-length nucleotide sequences of the virulent Trinidad donkey strain of
A:Reference number: A31467; MUID:69243175; PMID:2524126
A:Accession: B31467
A:Molecule type: mRNA
A:Residues: 1-1254 <K1>
A:Cross-references: UNIPROT:P09592; GB:J04332; NID:G2323708; PIDN:AAB02519.1; PID:G323710
R:Kinney, R.M.; Johnson, B.J.B.; Brown, V.L.; Trent, D.W.
Virology 152, 400-413, 1986
A:Title: Nucleotide sequence of the 26 S mRNA of the virulent Trinidad donkey strain of
A:Reference number: A47612; MUID:86263392; PMID:3089830
A:Accession: A47612
A:Molecule type: mRNA
A:Residues: 1-542, 'K', 544-810, 'P', 812-1254 <K12>
A:Cross-references: GB:L01442
C:Superfamily: togavirus structural polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-275/Product: coat protein #status predicted <CTP>
F:276-334/Product: membrane glycoprotein E3 #status predicted <MG3>
F:335-757/Product: membrane glycoprotein E2 #status predicted <MG2>
F:701-718/Domain: transmembrane #status predicted <TM1>
F:758-812/Product: 6K protein #status predicted <KP6>
F:774-790/Domain: transmembrane #status predicted <TM2>
F:795-813/Domain: transmembrane #status predicted <TM3>
F:813-1254/Product: membrane glycoprotein E1 #status predicted <MG1>
F:1231-1248/Domain: transmembrane #status predicted <TM4>
F:47,286,546,652,946/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match      25.8%; Score 58; DB 1; Length 1254;
Best Local Similarity 47.6%; Pred. No. 54;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 11 DVTWSSDGLWNNNQTLFLE 31
      : ||| |||||
Db 758 ETTWESLDHLWNNNQMFQ 778
      : ||| |||||

RESULT 8
B44213
structural polyprotein - Venezuelan equine encephalitis virus (strain P676)
N:Contains: 6K protein; coat protein; membrane glycoprotein E1; membrane glycoprotein E2
C:Species: Venezuelan equine encephalitis virus
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C:Accession: B44213
R:Kinney, R.M.; Teuchiya, K.R.; Snieder, J.M.; Trent, D.W.
Virology 191, 569-580, 1992
A:Title: Genetic evidence that epizootic Venezuelan equine encephalitis (VEE) viruses are
A:Reference number: A44213; MUID:93079859; PMID:1448915
A:Accession: B44213
A:Molecule type: genomic RNA
A:Residues: 1-1255 <K1N>
A:Cross-references: UNIPROT:P36332; GB:L04653; NID:G290609; PIDN:AAC19319.1; PID:G290611
C:Superfamily: togavirus structural polyprotein

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C;Keywords: late protein

DB 363 LYDVLDDNNVDITTEVEETPIGINIQSVFASEISTTIANIT 40

Search completed: June 23, 2003, 08:38:12
Job time : 4.70568 sec

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OM protein - protein search, using sw model

Run on: June 29, 2005, 09:46:27 ; Search time 49.0138 Seconds
(without alignments)
635.503 Million cell updates/sec

Title: US-10-718-321-6

Perfect score: 432

Sequence: 1 MPUPRONHEPVATSPSPQP.....NNOTQFLFLESLLTANTTKG 81

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 487488

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	99	22.9	18 17 US-10-718-321-1	Sequence 1, Appli
2	72	16.7	14 17 US-10-805-177-87	Sequence 87, Appl
3	67	15.5	12 17 US-10-805-177-92	Sequence 92, Appl
4	63	14.6	12 17 US-10-805-177-88	Sequence 88, Appl
5	60	13.9	50 9 US-09-864-761-40317	Sequence 40317, A
6	57	13.2	45 15 US-10-424-599-258666	Sequence 258666,
7	56	13.0	10 17 US-10-805-177-93	Sequence 93, Appl
8	56	13.0	47 16 US-10-425-115-195346	Sequence 195346,
9	54.5	12.6	40 16 US-10-481-180-489	Sequence 489, App
10	54.5	12.6	47 16 US-10-425-115-358602	Sequence 358602,
11	52.5	12.2	47 10 US-09-986-480-394	Sequence 394, App

12	52.5	12.2	47	16	US-10-425-115-354965	Sequence 354965,
13	52.5	12.2	47	17	US-10-863-332-394	Sequence 394, App
14	52.5	12.2	48	15	US-10-424-599-162113	Sequence 162113,
15	52	12.0	10	17	US-10-805-177-89	Sequence 89, Appl
16	52	12.0	47	14	US-10-029-386-32839	Sequence 32839, A
17	51.5	11.9	50	10	US-09-933-767-540	Sequence 540, App
18	51.5	11.9	50	14	US-10-004-860-540	Sequence 540, App
19	51.5	11.9	50	14	US-10-023-282-540	Sequence 540, App
20	50.5	11.7	47	15	US-10-424-599-272582	Sequence 272582,
21	50.5	11.7	47	15	US-10-424-599-272582	Sequence 272582,
22	48.5	11.2	41	16	US-10-425-115-312293	Sequence 312293,
23	48.5	11.2	42	15	US-10-424-599-283392	Sequence 283392,
24	48.5	11.2	45	16	US-10-425-115-232573	Sequence 232573,
25	48.5	11.2	48	14	US-10-008-524A-164	Sequence 164, App
26	48.5	11.2	48	15	US-10-350-719-164	Sequence 190016,
27	48	11.1	44	15	US-10-424-599-190016	Sequence 190016,
28	48	11.1	45	16	US-10-425-115-223316	Sequence 223316,
29	48	11.1	48	14	US-10-029-386-29088	Sequence 29088, A
30	48	11.1	48	15	US-10-424-599-28496	Sequence 28496,
31	48	11.1	49	15	US-10-424-599-192216	Sequence 192216,
32	48	11.1	50	16	US-10-425-115-256042	Sequence 256042,
33	47.5	11.0	40	15	US-10-424-599-264613	Sequence 264613,
34	47.5	11.0	40	16	US-10-425-115-352983	Sequence 352983,
35	47.5	11.0	46	16	US-10-425-115-203986	Sequence 203986,
36	47.5	11.0	50	11	US-09-864-408A-8636	Sequence 8636, Ap
37	47	10.9	8	17	US-10-805-177-104	Sequence 104, App
38	47	10.9	8	17	US-10-805-177-106	Sequence 106, App
39	47	10.9	10	17	US-10-805-177-98	Sequence 98, Appl
40	47	10.9	23	16	US-10-481-180-474	Sequence 474, App
41	47	10.9	47	16	US-10-437-963-174713	Sequence 174713,
42	47	10.9	47	16	US-10-425-115-188216	Sequence 188216,
43	46.5	10.8	34	16	US-10-425-115-309663	Sequence 309663,
44	46.5	10.8	44	15	US-10-424-599-208981	Sequence 208981,
45	46.5	10.8	46	10	US-09-764-891-5368	Sequence 5368, Ap

ALIGNMENTS

RESULT 1
US-10-718-321-1
; Sequence 1, Application US/10718321
; Publication No. US2005012117A1
; GENERAL INFORMATION:
; APPLICANT: Biogen Idec Ma Inc.
; APPLICANT: Bailly, Veronique
; APPLICANT: Bonventre, Joseph
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: Molecules and Methods for Inhibiting
; FILE REFERENCE: Shedding of KIM-1
; FILE REFERENCE: A124 US
; CURRENT APPLICATION NUMBER: US/10718,321
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/295449
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/295907
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US02/17402
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-718-321-1

Query Match 22.9%; Score 99; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 SSGGLWNNQTLFLEHS 72
|||||

Db 1 SSDGLMNNQTQLFLEHS 18

RESULT 2

US-10-805-177-87
 ; Sequence 87, Application US/10805177
 ; Publication No. US2005008449A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Landes, Gregory M.
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Bezabeh, Binyam
 ; APPLICANT: Foltz, Ian
 ; APPLICANT: Tse, Kam Fai
 ; APPLICANT: Jeffers, Michael
 ; APPLICANT: Mesri, Mehdi
 ; APPLICANT: Starling, Gary
 ; APPLICANT: Mezes, Peter
 ; APPLICANT: Khramtsov, Nikolai
 ; TITLE OF INVENTION: ANTIBODIES AGAINST T CELL IMMUNOGLOBULIN
 ; TITLE OF INVENTION: DOMAIN AND MUCIN DOMAIN 1 (TIM-1) ANTIGEN AND USES THEREOF
 ; FILE REFERENCE: ABXCUR.006A
 ; CURRENT APPLICATION NUMBER: US/10/805,177
 ; CURRENT FILING DATE: 2004-03-19
 ; PRIOR APPLICATION NUMBER: 60/456,652
 ; PRIOR FILING DATE: 2003-03-19
 ; NUMBER OF SEQ ID NOS: 141
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 87
 ; LENGTH: 14
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-805-177-87

Query Match 16.7%; Score 72; DB 17; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPLPRQNHEPVAT 13
 |||||
 Db 2 MPLPRQNHEPVAT 14

RESULT 3

US-10-805-177-92
 ; Sequence 92, Application US/10805177
 ; Publication No. US2005008449A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Landes, Gregory M.
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Bezabeh, Binyam
 ; APPLICANT: Foltz, Ian
 ; APPLICANT: Tse, Kam Fai
 ; APPLICANT: Jeffers, Michael
 ; APPLICANT: Mesri, Mehdi
 ; APPLICANT: Starling, Gary
 ; APPLICANT: Mezes, Peter
 ; APPLICANT: Khramtsov, Nikolai
 ; TITLE OF INVENTION: ANTIBODIES AGAINST T CELL IMMUNOGLOBULIN
 ; TITLE OF INVENTION: DOMAIN AND MUCIN DOMAIN 1 (TIM-1) ANTIGEN AND USES THEREOF
 ; FILE REFERENCE: ABXCUR.006A
 ; CURRENT APPLICATION NUMBER: US/10/805,177
 ; CURRENT FILING DATE: 2004-03-19
 ; PRIOR APPLICATION NUMBER: 60/456,652
 ; PRIOR FILING DATE: 2003-03-19
 ; NUMBER OF SEQ ID NOS: 141
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 92
 ; LENGTH: 12
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-805-177-92

Query Match 15.5%; Score 67; DB 17; Length 12;

Best Local Similarity 100.0%; Pred. No. 3;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPRQNHEPVAT 13
 |||||
 Db 1 PLPRQNHEPVAT 12

RESULT 4

US-10-805-177-88
 ; Sequence 88, Application US/10805177
 ; Publication No. US2005008449A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Landes, Gregory M.
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Bezabeh, Binyam
 ; APPLICANT: Foltz, Ian
 ; APPLICANT: Tse, Kam Fai
 ; APPLICANT: Jeffers, Michael
 ; APPLICANT: Mesri, Mehdi
 ; APPLICANT: Starling, Gary
 ; APPLICANT: Mezes, Peter
 ; APPLICANT: Khramtsov, Nikolai
 ; TITLE OF INVENTION: ANTIBODIES AGAINST T CELL IMMUNOGLOBULIN
 ; TITLE OF INVENTION: DOMAIN AND MUCIN DOMAIN 1 (TIM-1) ANTIGEN AND USES THEREOF
 ; FILE REFERENCE: ABXCUR.006A
 ; CURRENT APPLICATION NUMBER: US/10/805,177
 ; CURRENT FILING DATE: 2004-03-19
 ; PRIOR APPLICATION NUMBER: 60/456,652
 ; PRIOR FILING DATE: 2003-03-19
 ; NUMBER OF SEQ ID NOS: 141
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 88
 ; LENGTH: 12
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-805-177-88

Query Match 14.6%; Score 63; DB 17; Length 12;
 Best Local Similarity 100.0%; Pred. No. 7.7;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPLPRQNHEPV 11
 |||||
 Db 2 MPLPRQNHEPV 12

RESULT 5

US-09-864-761-40317
 ; Sequence 40317, Application US/09864761
 ; Patent No. US20020048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
 ; FILE REFERENCE: Aeomica-X-1
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/632,366
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30

; FEATURE: PAT MRT3847 755C.1.pcp
; OTHER INFORMATION: Clone ID:

US-10-423-113-193340

Matches 20; Conservative 4; Mismatches 16; Indels 7; Gaps 3;

Qy 13 TSPSPQAPAE--THPTTLOGAIRREPTSSPL-----YSTTDCNDTFTV 53
| | | | | : | | | | | : | | | | | : | | | | | :
Db 1 TSMSTTGPSETTTSPTTALTMSR-PTSMPLTWQKSYITISKFTVS 46
| | | | | : | | | | | : | | | | | : | | | | | :

RESULT 13

US-10-863-332-394
; Sequence 394, Application US/10863332
; Publication No. US20050064458A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 143 Human Secreted Proteins
; FILE REFERENCE: P5500P1
; CURRENT APPLICATION NUMBER: US/10/863,332
; CURRENT FILING DATE: 2004-06-09
; PRIOR APPLICATION NUMBER: US/09/986,480
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/12788
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/134,068
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 456
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 394
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (32)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (37)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-863-332-394

Query Match 12.2%; Score 52.5; DB 17; Length 47;
Best Local Similarity 35.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 2; Mismatches 13; Indels 7; Gaps 1;

Qy 7 NHEPVATSPSPQAPAEHTPTTLOGAIRREPTSSP 40
| | | | | : | | | | | : | | | | | : | | | | | :
Db 2 NMNPVSTLPLGSPSPSHTA-----HPPTPSP 28
| | | | | : | | | | | : | | | | | : | | | | | :

RESULT 14

US-10-424-599-162113
; Sequence 162113, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 162113
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_117405C.1.pep
US-10-424-599-162113

Query Match 12.2%; Score 52.5; DB 15; Length 48;
Best Local Similarity 31.5%; Pred. No. 4.8e+02;

Matches 17; Conservative 3; Mismatches 27; Indels 7; Gaps 1;

Qy 5 RQNEHPVATSPSPQAPAEHTPTTLOGAIRREPTSSPLSYTTDGNDTVTESD 58
| | | | | : | | | | | : | | | | | : | | | | | :
Db 1 RDXHEPVSPSPNSAAMS-----LGTINLVTFSSAQSRMVGVDVTAHPSTG 47
| | | | | : | | | | | : | | | | | : | | | | | :

RESULT 15

US-10-805-177-89
; Sequence 89, Application US/10805177
; Publication No. US20050084449A1
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Chen, Francine
; APPLICANT: Bezabeh, Binyam
; APPLICANT: Foltz, Ian
; APPLICANT: Tse, Kam Fai
; APPLICANT: Jeffers, Michael
; APPLICANT: Mesiri, Mehdi
; APPLICANT: Starling, Gary
; APPLICANT: Mezes, Peter
; APPLICANT: Khrantsov, Nikolai
; TITLE OF INVENTION: ANTIBODIES AGAINST T CELL IMMUNOGLOBULIN
; TITLE OF INVENTION: DOMAIN AND MUCIN DOMAIN 1 (TIM-1) ANTIGEN AND USES THEREOF
; FILE REFERENCE: ABXCUR.006A
; CURRENT APPLICATION NUMBER: US/10/805,177
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/456,652
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-805-177-89

Query Match 12.0%; Score 52; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPLPRQNH 9
| | | | | : | | | | | : | | | | | : | | | | | :
Db 2 MPLPRQNH 10
| | | | | : | | | | | : | | | | | : | | | | | :

Search completed: June 29, 2005, 10:14:18
Job time : 49.0138 secs

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OM protein - protein search, using sw model

Run on: June 29, 2005, 08:57:16 ; Search time 11.1395 Seconds
(without alignments)
542.805 Million cell updates/sec

Title: US-10-718-321-6
Perfect score: 432
Sequence: 1 MBLPRQNHVPATSPSPQ.....NNQTLFLEHSLLTANTTKG 81

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents:AA:*
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3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	432	100.0	334	US-09-197-970B-7	Sequence 7, Appli
2	348	80.6	451	US-08-287-001A-2	Sequence 2, Appli
3	348	80.6	451	PCT-US95-09941-2	Sequence 2, Appli
4	89	20.6	307	US-09-197-970B-3	Sequence 3, Appli
5	71.5	16.6	297	US-09-006-535-4	Sequence 4, Appli
6	71	16.4	1911	US-09-854-856-64	Sequence 64, Appli
7	71	16.4	1939	US-09-854-856-48	Sequence 48, Appli
8	71	16.4	1371	US-09-854-856-32	Sequence 32, Appli
9	71	16.4	1999	US-09-854-856-16	Sequence 16, Appli
10	71	16.4	2004	US-09-854-856-58	Sequence 58, Appli
11	71	16.4	2032	US-09-854-856-42	Sequence 42, Appli
12	71	16.4	2048	US-09-854-856-62	Sequence 62, Appli
13	71	16.4	2064	US-09-854-856-26	Sequence 26, Appli
14	71	16.4	2076	US-09-854-856-46	Sequence 46, Appli
15	71	16.4	2092	US-09-854-856-10	Sequence 10, Appli
16	71	16.4	2108	US-09-854-856-30	Sequence 30, Appli
17	71	16.4	2136	US-09-854-856-14	Sequence 14, Appli
18	71	16.4	2141	US-09-854-856-56	Sequence 56, Appli
19	71	16.4	2157	US-09-854-856-52	Sequence 52, Appli
20	71	16.4	2169	US-09-854-856-40	Sequence 40, Appli
21	71	16.4	2185	US-09-854-856-36	Sequence 36, Appli
22	71	16.4	2201	US-09-854-856-24	Sequence 24, Appli
23	71	16.4	2217	US-09-854-856-20	Sequence 20, Appli
24	71	16.4	2229	US-09-854-856-8	Sequence 8, Appli
25	71	16.4	2245	US-09-854-856-4	Sequence 4, Appli
26	71	16.4	2294	US-09-854-856-50	Sequence 50, Appli
27	71	16.4	2322	US-09-854-856-34	Sequence 34, Appli

28	71	16.4	2354	4	US-09-854-856-18	Sequence 18, Appli
29	71	16.4	2382	4	US-09-854-856-2	Sequence 2, Appli
30	70	16.2	109	4	US-09-270-767-46395	Sequence 46395, A
31	69.5	16.1	196	4	US-09-248-796A-17562	Sequence 17562, A
32	69.5	16.1	445	2	US-08-900-148-2	Sequence 2, Appli
33	69.5	16.1	479	4	US-09-248-796A-20593	Sequence 20593, A
34	69	16.0	567	4	US-09-514-245-6	Sequence 6, Appli
35	69	16.0	602	1	US-08-168-091A-2	Sequence 2, Appli
36	69	16.0	602	1	US-08-428-926-5	Sequence 5, Appli
37	69	16.0	602	1	US-08-428-927-5	Sequence 5, Appli
38	69	16.0	602	1	US-08-428-298-5	Sequence 5, Appli
39	69	16.0	602	1	US-08-339-517-5	Sequence 5, Appli
40	69	16.0	1070	3	US-08-697-954-2	Sequence 2, Appli
41	69	16.0	1166	4	US-09-200-650E-7	Sequence 7, Appli
42	68.5	15.9	319	4	US-09-270-767-44343	Sequence 44343, A
43	68.5	15.9	681	3	US-08-760-615-4	Sequence 4, Appli
44	68.5	15.9	681	4	US-09-336-910A-2	Sequence 2, Appli
45	67.5	15.6	160	4	US-09-270-767-46213	Sequence 46213, A

ALIGNMENTS

RESULT 1
US-09-197-970B-7
; Sequence 7, Application US/09197970B
; Patent No. 6664385
; GENERAL INFORMATION:
; APPLICANT: Michele Sanicola-Nadel
; Joseph V. Bonventre
; Catherine A. Hession
; Takaharu Ichimura
; Henry Wei
; Richard L. Cate
; TITLE OF INVENTION: MODULATORS OF TISSUE REGENERATION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/197,970B
; FILING DATE: 23-No. 6664385-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/018,228
; FILING DATE: 24-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Levine, Leslie M.
; REGISTRATION NUMBER: 35,245
; REFERENCE/DOCKET NUMBER: A010 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 679-2810
; TELEFAX: (617) 679-2838
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 334 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-197-970B-7
Query Match 100.0%; Score 432; DB 4; Length 334;
Best Local Similarity 100.0%; Pred. NO. 2e-41;

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Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFLPRQNHVPATSPSPQPAETHPTTLOGAIRREPTSSPLSYTTDGNMTVTSSDGLW 60
Db 210 MFLPRQNHVPATSPSPQPAETHPTTLOGAIRREPTSSPLSYTTDGNMTVTSSDGLW 269
QY 61 NNNQTLFLEHSLLTANTTKG 81
Db 270 NNNQTLFLEHSLLTANTTKG 290

RESULT 2
US-08-287-001A-2
; Sequence 2, Application US/08287001A
; Patent No. 5622861
; GENERAL INFORMATION:
; APPLICANT: KAPLAN, GERARDO
; APPLICANT: FEINSTONE, STEPHEN M.
; TITLE OF INVENTION: HEPATITIS A VIRUS RECEPTOR AND METHODS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, The Candler Bldg, 127 Peachtree
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/287,001A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Spratt, Gwedolyn D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 1414.621
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-287-001A-2
Query Match 80.6%; Score 348; DB 1; Length 451;
Best Local Similarity 82.5%; Pred. No. 1.2e-31;
Matches 66; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
QY 2 PLPRQNHVPATSPSPQPAETHPTTLOGAIRREPTSSPLSYTTDGNMTVTSSDGLW 61
Db 291 PLPMQNHVPATSPSPQPAETHPTTLOGAIRREPTSSPLSYTTDGNMTVTSSDGLW 350
QY 62 NNNQTLFLEHSLLTANTTKG 81
Db 351 NNNQTLSPHSPQMVNTTEG 370

RESULT 3
PCT-US95-09941-2
; Sequence 2, Application PC/TUS9509941
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HEPATITIS A VIRUS RECEPTOR AND METHODS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, The Candler Bldg, 127 Peachtree
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09941
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/287,001
; FILING DATE: 5 AUG 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Spratt, Gwedolyn D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 1414.621
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-287-001A-2
Query Match 80.6%; Score 348; DB 1; Length 451;
Best Local Similarity 82.5%; Pred. No. 1.2e-31;
Matches 66; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
QY 2 PLPRQNHVPATSPSPQPAETHPTTLOGAIRREPTSSPLSYTTDGNMTVTSSDGLW 61
Db 291 PLPMQNHVPATSPSPQPAETHPTTLOGAIRREPTSSPLSYTTDGNMTVTSSDGLW 350
QY 62 NNNQTLFLEHSLLTANTTKG 81
Db 351 NNNQTLSPHSPQMVNTTEG 370

RESULT 4
US-09-197-970B-3
; Sequence 3, Application US/09197970B
; Patent No. 6664385
; GENERAL INFORMATION:
; APPLICANT: Michele Sanicola-Nadel
; APPLICANT: Joseph V. Bonventre
; APPLICANT: Catherine A. Hession
; APPLICANT: Takaharu Ichimura
; APPLICANT: Henry Wei
; APPLICANT: Richard L. Cate
; TITLE OF INVENTION: MODULATORS OF TISSUE REGENERATION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, The Candler Bldg, 127 Peachtree
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09941
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/287,001
; FILING DATE: 5 AUG 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Spratt, Gwedolyn D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 1414.621
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-09941-2
Query Match 80.6%; Score 348; DB 5; Length 451;
Best Local Similarity 82.5%; Pred. No. 1.2e-31;
Matches 66; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
QY 2 PLPRQNHVPATSPSPQPAETHPTTLOGAIRREPTSSPLSYTTDGNMTVTSSDGLW 61
Db 291 PLPMQNHVPATSPSPQPAETHPTTLOGAIRREPTSSPLSYTTDGNMTVTSSDGLW 350
QY 62 NNNQTLFLEHSLLTANTTKG 81
Db 351 NNNQTLSPHSPQMVNTTEG 370

RESULT 4
US-09-197-970B-3
; Sequence 3, Application US/09197970B
; Patent No. 6664385
; GENERAL INFORMATION:
; APPLICANT: Michele Sanicola-Nadel
; APPLICANT: Joseph V. Bonventre
; APPLICANT: Catherine A. Hession
; APPLICANT: Takaharu Ichimura
; APPLICANT: Henry Wei
; APPLICANT: Richard L. Cate
; TITLE OF INVENTION: MODULATORS OF TISSUE REGENERATION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/197,970B
FILING DATE: 23-NO. 6664385-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/018,228
FILING DATE: 24-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Levine, Leslie M.
REGISTRATION NUMBER: 35,245
REFERENCE/DOCKET NUMBER: A010 PCT CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 679-2810
TELEFAX: (617) 679-2838
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-197-970B-3

Query Match 20.8%; Score 89; DB 4; Length 307;
Best Local Similarity 34.1%; Pred. No. 0.036;
Matches 31; Conservative 9; Mismatches 27; Indels 24; Gaps 6;
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DB 155 RSTHVTSTRVSTSTPSTPSTQTHKEITTFYAHETT-----AEVTETPSYT-PADWNG 207
QY 51 TVTESDGLWNNNQTLFLEHSLLTANTTKG 81
DB 208 TWT-SSEAWNHTVPLRKP--QRNPTKG 235

RESULT 5
US-09-006-535-4
Sequence 4, Application US/09006535
Patent No. 5965396
GENERAL INFORMATION:
APPLICANT: Julie Yan Pan
APPLICANT: Mark Egerton
APPLICANT: David Shay Silberstein
TITLE OF INVENTION: HUMAN LYPH NODE DERIVED GTPase
FILE REFERENCE: PHM 70295
CURRENT APPLICATION NUMBER: US/09/006,535
PRIOR FILING DATE: 1998-01-13
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
TYPE: PRT
ORGANISM: Mus musculus
US-09-006-535-4

Query Match 16.6%; Score 71.5; DB 2; Length 297;
Best Local Similarity 30.6%; Pred. No. 3.5;
Matches 19; Conservative 9; Mismatches 27; Indels 7; Gaps 3;
QY 1 MPLPRQNHPP--VATSPSPQPAETHPTTLOGAIRREPTSSPLYSTTGDNDTVTSSDG 58
DB 21 LPLSSRGHPGRLCTAPSAP---SQHPLGQSVSLNPPVRKP--SPAQDGSSESSESDSG 75
QY 59 LW 60
DB 76 SW 77

RESULT 6
US-09-854-856-64
Sequence 64, Application US/09854856

Patent No. 6541252
GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Hilbun, Erin
APPLICANT: Donoho, Gregory
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides
FILE REFERENCE: LEX-0178-USA
CURRENT APPLICATION NUMBER: US/09/854,856
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: US 60/206,015
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 64
LENGTH: 1911
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(1911)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-854-856-64

Query Match 16.4%; Score 71; DB 4; Length 1911;
Best Local Similarity 39.6%; Pred. No. 46;
Matches 19; Conservative 7; Mismatches 16; Indels 6; Gaps 2;
QY 9 EPVATSPSPQPAETHPTTLOGAIRREPTSSPLYSTTGDNDTVTSS 56
DB 715 EPVAVA---QPQATQPTTLASSV--DSAHSDVASGMSDGNENVPSS 756

RESULT 7
US-09-854-856-48
Sequence 48, Application US/09854856
Patent No. 6541252
GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Hilbun, Erin
APPLICANT: Donoho, Gregory
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides
FILE REFERENCE: LEX-0178-USA
CURRENT APPLICATION NUMBER: US/09/854,856
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: US 60/206,015
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 48
LENGTH: 1939
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(1939)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-854-856-48

Query Match 16.4%; Score 71; DB 4; Length 1939;
Best Local Similarity 39.6%; Pred. No. 47;
Matches 19; Conservative 7; Mismatches 16; Indels 6; Gaps 2;
QY 9 EPVATSPSPQPAETHPTTLOGAIRREPTSSPLYSTTGDNDTVTSS 56
DB 743 EPVAVA---QPQATQPTTLASSV--DSAHSDVASGMSDGNENVPSS 784

RESULT 8
US-09-854-856-32

898 Db

Search completed: June 29, 2005, 09:02:56
Job time : 12.1395 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 09:46:27 ; Search time 31.4656 Seconds
(without alignments)

635.503 Million cell updates/sec

Title: US-10-718-321-7_COPY_249_300

Perfect score: 275

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Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 487488

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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19: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	48	17.5	38	16	US-10-425-115-199618	Sequence 199618,
3	48	17.5	44	15	US-10-424-599-190016	Sequence 190016,
4	48	17.5	48	15	US-10-424-599-282496	Sequence 282496,
5	47.5	17.3	40	15	US-10-424-599-264613	Sequence 264613,
6	47	17.1	44	14	US-10-321-857-22	Sequence 22, Appl
7	47	17.1	44	14	US-10-318-675-22	Sequence 22, Appl
8	46	16.7	44	15	US-10-424-599-240616	Sequence 240616,
9	46	16.7	49	15	US-10-424-599-179504	Sequence 179504,
10	45	16.4	37	10	US-09-983-802-399	Sequence 399, App
11	45	16.4	37	10	US-09-984-490-399	Sequence 399, App

12	45	16.4	37	11	US-09-973-278-509	Sequence 509, App
13	43.5	15.8	31	15	US-10-424-599-284397	Sequence 284397,
14	43.5	15.8	42	16	US-10-437-963-166786	Sequence 166786,
15	43.5	15.8	44	16	US-10-437-963-195017	Sequence 195017,
16	43.5	15.8	48	15	US-10-424-599-151333	Sequence 151333,
17	43	15.6	43	9	US-09-925-300-1031	Sequence 1031, Ap
18	42.5	15.5	43	16	US-10-425-115-191318	Sequence 191318,
19	42.5	15.5	45	15	US-10-424-599-152970	Sequence 152970,
20	42.5	15.5	47	16	US-10-425-115-338727	Sequence 338727,
21	42	15.3	35	15	US-10-424-599-216152	Sequence 216152,
22	42	15.3	42	15	US-10-424-599-265756	Sequence 265756,
23	42	15.3	42	16	US-10-425-115-335582	Sequence 335582,
24	42	15.3	47	15	US-10-424-599-277738	Sequence 277738,
25	42	15.3	50	16	US-10-425-115-367358	Sequence 367358,
26	41.5	15.1	37	15	US-10-424-599-269343	Sequence 269343,
27	41.5	15.1	42	15	US-10-424-599-274203	Sequence 274203,
28	41.5	15.1	43	14	US-10-321-857-117	Sequence 117, App
29	41.5	15.1	43	14	US-10-318-675-117	Sequence 117, App
30	41	14.9	30	10	US-09-974-879-549	Sequence 549, App
31	41	14.9	30	10	US-09-305-736-554	Sequence 554, App
32	41	14.9	30	10	US-09-818-683-554	Sequence 554, App
33	41	14.9	30	11	US-09-818-683-554	Sequence 554, App
34	41	14.9	30	15	US-10-621-401-549	Sequence 549, App
35	41	14.9	32	16	US-10-425-115-328576	Sequence 328576,
36	41	14.9	37	16	US-10-425-115-330334	Sequence 330334,
37	41	14.9	39	9	US-09-984-245-123	Sequence 123, App
38	41	14.9	39	10	US-09-966-262-123	Sequence 123, App
39	41	14.9	39	10	US-09-983-966-123	Sequence 123, App
40	41	14.9	39	14	US-10-059-395-123	Sequence 123, App
41	41	14.9	39	14	US-10-143-090-123	Sequence 123, App
42	41	14.9	39	16	US-10-425-115-194419	Sequence 194419,
43	41	14.9	39	16	US-10-608-029-29	Sequence 29, Appl
44	41	14.9	39	17	US-10-960-251-123	Sequence 123, App
45	41	14.9	47	15	US-10-424-599-263904	Sequence 263904,

ALIGNMENTS

RESULT 1
US-10-718-321-1
; Sequence 1, Application US/10718321
; Publication NO. US20050112117A1
; GENERAL INFORMATION:
; APPLICANT: Biogen Idec Ma Inc.
; APPLICANT: Bailly, Veronique
; APPLICANT: Bonventre, Joseph
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: Molecules and Methods for Inhibiting
; TITLE OF INVENTION: Shedding of KIM-1
; FILE REFERENCE: A124 US
; CURRENT APPLICATION NUMBER: US/10718,321
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/295449
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/295907
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US02/17402
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-718-321-1

Query Match 36.0%; Score 99; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 SSDGLWNNQTFLEHS 33
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Db      1  SSDGLWNNQTQFLFLEHS 18

RESULT 2
US-10-425-115-199618
; Sequence 199618, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 199618
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_113624C.1.pep
US-10-425-115-199618

Query Match      17.5%; Score 48; DB 16; Length 38;
Best Local Similarity 33.3%; Pred. No. 68;
Matches 10; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

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Db      6  NNKTQFNSSVIIVSSNHGITINLSIAL 35

RESULT 3
US-10-424-599-190016
; Sequence 190016, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 190016
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_142603C.1.pep
US-10-424-599-190016

Query Match      17.5%; Score 48; DB 15; Length 44;
Best Local Similarity 37.9%; Pred. No. 81;
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RESULT 4
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; Sequence 282496, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J

Db      1  SSDGLWNNQTQFLFLEHS 18

RESULT 2
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; Sequence 199618, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 199618
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_113624C.1.pep
US-10-425-115-199618

Query Match      17.5%; Score 48; DB 16; Length 38;
Best Local Similarity 33.3%; Pred. No. 68;
Matches 10; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY      23  NNQTQFLFLEHSLTANTTKGIYAGVCISVL 52
Db      6  NNKTQFNSSVIIVSSNHGITINLSIAL 35

RESULT 3
US-10-424-599-190016
; Sequence 190016, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 190016
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_142603C.1.pep
US-10-424-599-190016

Query Match      17.5%; Score 48; DB 15; Length 44;
Best Local Similarity 37.9%; Pred. No. 81;
Matches 11; Conservative 7; Mismatches 7; Indels 4; Gaps 1;

QY      12  TVTSSDGLWNN-----QTQFLFLEHSLT 36
Db      2  TPTQSSLNIFYHNTSLSETSFPIKHSLT 30

RESULT 4
US-10-424-599-282496
; Sequence 282496, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J

Db      1  SSDGLWNNQTQFLFLEHS 18

RESULT 2
US-10-425-115-199618
; Sequence 199618, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 282496
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_97115C.1.pep
US-10-424-599-282496

Query Match      17.5%; Score 48; DB 15; Length 48;
Best Local Similarity 39.3%; Pred. No. 91;
Matches 11; Conservative 3; Mismatches 8; Indels 6; Gaps 1;

QY      20  LWNNNQTQFLFLEHSLT-----NTTK 41
Db      7  MWKNRQTKSFLERHVLPGMSQHYRNLT 34

RESULT 5
US-10-424-599-264613
; Sequence 264613, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 264613
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_80967C.1.pep
US-10-424-599-264613

Query Match      17.3%; Score 47.5; DB 15; Length 40;
Best Local Similarity 40.0%; Pred. No. 84;
Matches 12; Conservative 3; Mismatches 10; Indels 5; Gaps 1;

QY      11  DVTSSDGLWNNQTQFLFLEHSLTANTT 40
Db      7  ETHTELDSPLAQNNNLFI-----LTATTS 31

RESULT 6
US-10-321-857-22
; Sequence 22, Application US/10321857
; Publication No. US20030180816A1
; GENERAL INFORMATION:
; APPLICANT: Applied NanoSystems B.V.
; TITLE OF INVENTION: A method to provide bacterial ghosts with antigens
; FILE REFERENCE: 2183-5547US
; CURRENT APPLICATION NUMBER: US/10/321,857
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/NL02/00383
; PRIOR FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: 01202239.8
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 165
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RESULT 8
US-10-424-599-240616
Sequence 240616, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovacic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 240616
LENGTH: 44
TYPE: PRT

```

1  APPLICANT: CAO Tongwei
2  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
3  TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
4  FILE REFERENCE: 38-21(53223)B
5  CURRENT APPLICATION NUMBER: US/10/424,599
6  CURRENT FILING DATE: 2003-04-28
7  NUMBER OF SEQ ID NOS: 285684
8  SEQ ID NO 240616
9  LENGTH: 44
10 TYPE: PRT

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RESULT	10
US-09-983-802-399	
, Sequence 399, Application US/09983802	
, Publication No. US20030022185A1	
, GENERAL INFORMATION:	
, APPLICANT: Fischer et al.	
, TITLE OF INVENTION: 123 Human Secreted Proteins	
, FILE REFERENCE: PZ010P1	
, CURRENT APPLICATION NUMBER: US/09/983,802	
, CURRENT FILING DATE: 2001-10-25	
, PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/227,357	
, PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-08	
, PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/1	
, PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-07	
, PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,926	
, PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08	
, PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,793	
, PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08	
, PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,925	
, PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08	
, PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,929	
, PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08	
, PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,803	
, PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08	
, PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,732	
, PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08	
, PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,931	


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; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 399
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-490-399

Query Match      16.4%; Score 45; DB 10; Length 37;
Best Local Similarity 27.3%; Pred. No. 1.7e+02;
Matches 9; Conservative 7; Mismatches 13; Indels 4; Gaps 1;

QY 20 LWNNTQQLFLEHSLTANTTKGIYAGVCISVL 52
    ||||| : ||:: : |::|
Db 3 LWNRNQ----MMHSIIVKELIVTFELGITVLL 31

RESULT 12
US-09-973-278-509
; Sequence 509, Application US/09973278
; Publication No. US20040044191A1
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: PZ010P2
; CURRENT APPLICATION NUMBER: US/09/973,278
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 60/239,899
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 09/227,357
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/13684
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/051,926
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/052,793
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,925
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,929
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/052,803
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/052,732
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,931
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,932
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,916
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,930
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,918
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,920
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/052,733
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/052,795
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,919
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,928
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/055,722
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,723
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,948
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,949
; PRIOR FILING DATE: 1997-08-18

; PRIOR APPLICATION NUMBER: 60/055,953
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,950
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,947
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,964
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/056,360
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,684
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,984
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,954
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/058,785
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,664
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,660
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,661
; PRIOR FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 509
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-278-509

Query Match      16.4%; Score 45; DB 11; Length 37;
Best Local Similarity 27.3%; Pred. No. 1.7e+02;
Matches 9; Conservative 7; Mismatches 13; Indels 4; Gaps 1;

QY 20 LWNNTQQLFLEHSLTANTTKGIYAGVCISVL 52
    ||||| : ||:: : |::|
Db 3 LWNRNQ----MMHSIIVKELIVTFELGITVLL 31

RESULT 13
US-10-424-599-284397
; Sequence 284397, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 284397
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_98836C.1.pap
US-10-424-599-284397

Query Match      15.8%; Score 43.5; DB 15; Length 31;
Best Local Similarity 37.5%; Pred. No. 2.1e+02;
Matches 9; Conservative 7; Mismatches 5; Indels 3; Gaps 1;

QY 21 WNNNOT---QLFLEHSLTANTTK 41
    |::| : ||::| : ||::|
Db 5 WDNSTYLVQPILENQLLSLSASK 28
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Job time : 32.4656 secs

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RESULT 14
US-10-437-963-166786
; Sequence 166786, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 166786
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_65460C.1.pap
US-10-437-963-166786

Query Match      15.8%; Score 43.5; DB 16; Length 42;
Best Local Similarity 47.8%; Pred. No. 3.1e+02;
Matches 11; Conservative 6; Mismatches 3; Indels 3; Gaps 2;

QY      20 LWNNTQTLF-LHESLLTANTTK 41
DB      15 IWTNLTKLYLLKHTLL--NSTK 35

RESULT 15
US-10-437-963-195017
; Sequence 195017, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 195017
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_91005C.1.pap
US-10-437-963-195017

Query Match      15.8%; Score 43.5; DB 16; Length 44;
Best Local Similarity 35.3%; Pred. No. 3.3e+02;
Matches 12; Conservative 8; Mismatches 11; Indels 3; Gaps 2;

QY      21 WNNNTQLFLEHSL--LTANTTKGIYAGVCISVL 52
DB      3 WHSLPDEVW-EHALSFLPADADRGAAAGACTSWL 35

Search completed: June 29, 2005, 10:14:20
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Result No.	Score	Match	Query	DB	ID	Description
1	52.5	19.1	30	4	US-09-282-029A-470	Sequence 470, App
2	52.5	19.1	30	4	US-09-282-029A-471	Sequence 471, App
3	52.5	19.1	30	4	US-09-434-355A-470	Sequence 470, App
4	52.5	19.1	30	4	US-09-434-355A-471	Sequence 471, App
5	45.5	16.5	40	1	US-08-188-228-22	Sequence 22, Appl
6	45.5	16.5	40	1	US-08-332-643-22	Sequence 22, Appl
7	45.5	16.5	40	1	US-08-332-638-22	Sequence 22, Appl
8	45	16.4	37	3	US-09-227-357-399	Sequence 399, App
9	44.5	16.2	31	3	US-08-190-802A-244	Sequence 244, App
10	44.5	16.2	31	3	US-08-477-346-244	Sequence 244, App
11	44.5	16.2	31	3	US-08-477-389-244	Sequence 244, App
12	44.5	16.2	31	3	US-08-487-072A-244	Sequence 244, App
13	44	16.0	40	1	US-08-218-025A-65	Sequence 65, Appl
14	42	15.3	40	1	US-08-188-228-16	Sequence 16, Appl
15	42	15.3	40	1	US-08-332-643-16	Sequence 16, Appl
16	42	15.3	40	1	US-08-332-638-16	Sequence 16, Appl
17	41.5	15.1	32	2	US-08-708-620A-4	Sequence 4, Appl
18	41	14.9	42	4	US-09-434-355A-529	Sequence 529, App
19	40	14.5	14	4	US-09-570-921-141	Sequence 141, App
20	40	14.5	42	4	US-09-282-029A-6	Sequence 6, Appl
21	40	14.5	42	4	US-09-185-908-6	Sequence 6, Appl
22	40	14.5	42	4	US-09-434-355A-6	Sequence 6, Appl
23	40	14.5	49	3	US-09-217-228-9	Sequence 9, Appl
24	39.5	14.4	30	1	US-08-190-802A-123	Sequence 123, App
25	39.5	14.4	30	3	US-08-477-346-123	Sequence 123, App
26	39.5	14.4	30	3	US-08-473-089-123	Sequence 123, App
27	39.5	14.4	30	4	US-08-487-072A-123	Sequence 123, App


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US-08-473-089--244
; Sequence 244, Application US/08473089
; Patent No. 6342368
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,089
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 244:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: YCU7 rI, Fig. 48
;
US-08-473-089--244

Query Match          16.2%; Score 44.5; DB 3; Length
Best Local Similarity 40.9%; Pred. No. 44;
Matches           9; Conservative      5; Mismatches    5; Indels     1

OY       4 SYTTDGNVTVESDG---LWN 22
         :|::||:|||::||::||::|
Db        10 AYSFDGSRVVTASEDKIKWVD 31

RESULT 12
US-08-487-072A-244
; Sequence 244, Application US/08487072A
; Patent No. 6423684
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,072A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 244:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: YCU7 rI, Fig. 48
; US-08-487-072A-244

Query Match 16.2%; Score 44.5; DB 4; Length 31;
Best Local Similarity 40.9%; Pred. No. 44;
Matches 9; Conservative 5; Mismatches 5; Indels 3;

QY 4 SYTTGNDTVTSSDG--LWN 22
Db 10 AYSFGSRVVTASEDGKIKVWD 31

RESULT 13
US-08-218-025A-65
; Sequence 65, Application US/08218025A
; Patent No. 5556744
; GENERAL INFORMATION:
; APPLICANT: Weiner, David B.
; APPLICANT: Ugen, Kenneth E.
; APPLICANT: Williams, William V.
; TITLE OF INVENTION: Methods and Compositions for Diagnosing
; TITLE OF INVENTION: and Treating Certain HIV Infected Patients
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: P.O. Box 457, 321 No. 5556744ristown Road
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/218,025A
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/891,451
; FILING DATE: 29-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST33A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9206
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-218-025A-65

Query Match 16.0%; Score 44; DB 1; Length 20;
Best Local Similarity 39.1%; Pred. No. 29;
Matches 9; Conservative 4; Mismatches 2; Indels 8; Gaps 1;

QY 1 LYSYTTDGDNTVTSSDGLWNN 23
||:|:|:|:|:|:|
DB 2 PLFNSTWNGNNT-----WNN 16

RESULT 14

US-08-188-228-16
; Sequence 16, Application US/08188228
; Patent No. 5597725

; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,228

; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/049,460
; FILING DATE: 19 APR 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,643

; FILING DATE: 17 APR 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5597725and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448

; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-188-228-16

Query Match 15.3%; Score 42; DB 1; Length 40;
Best Local Similarity 39.1%; Pred. No. 1.3e+02;
Matches 9; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 2 LYSYTTDGDNTVTSSDGLWNN 24
|:|:|:|:|:|:|:|:|:|
DB 2 LQYAFEGNGSVAESLSLSDNS 24

RESULT 15

US-08-332-643-16

; Sequence 16, Application US/08332643
; Patent No. 5639634
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two first National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,643

; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/872,643

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5639634and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740

; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-332-643-16

Query Match 15.3%; Score 42; DB 1; Length 40;
Best Local Similarity 39.1%; Pred. No. 1.3e+02;
Matches 9; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 2 LYSYTTDGDNTVTSSDGLWNN 24
|:|:|:|:|:|:|:|:|:|
DB 2 LQYAFEGNGSVAESLSLSDNS 24

Search completed: June 29, 2005, 09:49:08
Job time : 9.39882 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 09:03:05 ; Search time 35.5521 Seconds
(without alignments)
565.693 Million cell updates/sec

Title: US-10-718-321-7_COPY_249_300
Perfect score: 275
Sequence: 1 PLYSVTTGNDVTFTSSDGL.....SLLTANTTKGIYAGVCIISVL 52

Scoring table: BLASTSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 938430

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	36.7	18	6	AAO26686 Human KIM
2	99	36.0	18	6	AAO26687 Human KIM
3	99	36.0	18	6	AAO26673 Monoclonal
4	90	32.7	18	6	AAO26688 Human KIM
5	82	29.8	18	6	AAO26685 Human KIM
6	49	17.8	43	6	ADA98306 Human sec
7	49	17.8	43	6	ADA44132 Human sec
8	49	17.8	43	7	ADC20470 Human sec
9	49	17.8	43	7	ADFI0760 Human sec
10	49	17.8	44	3	AA829810 Human sec
11	48.5	17.6	40	8	AD507403 Staphyloc
12	47	17.1	44	2	AAI13969 Lys repea
13	47	17.1	44	6	ABR83729 Bacteriop
14	47	17.1	44	7	ADF70020 Acma-type
15	46	16.7	49	4	AAW92081 Human dig
16	45.5	16.5	40	2	AAW25651 Rat cadhe
17	45.5	16.5	40	2	AAW13116 Rat cadhe
18	45	16.4	37	7	ADA07578 Human sec
19	45	16.4	37	8	ADN41387 Novel hum
20	44.5	16.2	31	2	AA885818 Peptide r
21	44	16.0	20	2	AAW08045 HIV pepti
22	44	16.0	44	7	ADF70018 Acma-type
23	43	15.6	43	3	AA856453 Human pro
24	42.5	15.5	20	8	AD195222 OSPF-rela
25	42	15.3	40	2	AA843565 Rat cadhe

26	42	15.3	40	2	AAW25648 Rat cadhe
27	42	15.3	40	2	AAW13113 Rat cadhe
28	42	15.3	46	7	ADF70089 Acma-type
29	42	15.3	49	2	AA883059 Human IL-
30	41.5	15.1	32	2	AAW18789 Z peptide
31	41.5	15.1	43	6	ABR83824 Bacillus
32	41.5	15.1	43	7	ADF69876 Acma-type
33	41.5	15.1	49	2	AA861126 Vasoactiv
34	41	14.9	30	6	ABO14381 Novel hum
35	41	14.9	30	8	ADG78793 Human sec
36	41	14.9	30	8	ADN61079 Human sec
37	41	14.9	39	2	AAW67809 Human sec
38	41	14.9	46	4	AAW24315 Rat EST e
39	41	14.9	46	7	ADF60572 Human con
40	41	14.9	46	7	ADF59574 Human pol
41	41	14.9	49	1	AA891538 Modified
42	41	14.9	50	5	ABP11026 Human ORF
43	40.5	14.7	50	4	ABG30194 Novel hum
44	40	14.5	14	7	AD803490 BGS-3 asp
45	40	14.5	14	8	ADO10179 Human int

ALIGNMENTS

RESULT 1
AAO26686
ID AAO26686 standard; peptide; 18 AA.
XX
AC AAO26686;
XX
DT 20-MAR-2003 (first entry)
XX
DE Human KIM-1 mucin domain related peptide, SEQ ID No 14.
XX
KW Cytostatic; gene therapy; antibody; antigen; antigen-binding;
KW proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;
KW renal disease; injury; renal cancer.
XX
OS Synthetic.
XX
PN WO200298920-A1.
XX
PD 12-DEC-2002.
XX
PF 31-MAY-2002; 2002WO-US017402.
XX
PR 01-JUN-2001; 2001US-0295449P.
PR 04-JUN-2001; 2001US-0295907P.
(BIOJ) BIOGEN INC.
(GEHO) GEN HOSPITAL CORP.
PI Bailly V, Bonventre J;
XX
DR WPI; 2003-156845/15.
XX
PT New antibody, antibody derivative or antigen-binding polypeptide that
PT inhibits proteolytic release of a soluble kidney injury molecule-1
PT polypeptide, useful for treating or preventing renal disease or injury,
e.g. renal cancer.
XX
PS Disclosure; Fig 1A; 42pp; English.
XX
CC The invention relates to a novel antibody, antibody derivative or antigen
CC -binding polypeptide that inhibits proteolytic release of a soluble
CC kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.
CC The antibody, antibody derivative or antigen-binding polypeptide is
CC useful for treating or preventing renal disease or injury, e.g. renal
CC cancer. The antibody is also useful for inhibiting shedding of the KIM-1
CC polypeptide. This sequence represents a human KIM-1 mucin domain related
XX peptide of the invention

```

SQ Sequence 18 AA;
  Query Match          36.7%; Score 101; DB 6; Length 18;
  Best Local Similarity 100.0%; Pred. No. 1.4e-05;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 7 TDGNDTVTESSDGLWNNN 24
  DB 1 TDGNDTVTESSDGLWNNN 18

RESULT 2
AAO26687
ID AAO26687 standard; peptide; 18 AA.
AC AAO26687;
XX
XX 20-MAR-2003 (first entry)
XX Human KIM-1 mucin domain related peptide, SEQ ID No 15.
DE
DE Human KIM-1 mucin domain related peptide, SEQ ID No 15.
XX
XX Cytostatic; gene therapy; antibody; antigen; antigen-binding;
KW proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;
KW renal disease; injury; renal cancer.
XX
XX Synthetic.
OS
XX WO200298920-A1.
PN
XX 12-DEC-2002.
PD
XX 31-MAY-2002; 2002WO-US017402.
PF
XX 01-JUN-2001; 2001US-0295449P.
PR 04-JUN-2001; 2001US-0295907P.
XX
XX (BIOJ ) BIOGEN INC.
PA (GEO ) GEN HOSPITAL CORP.
XX
XX Baillly V, Bonventre J;
PI
XX WPI; 2003-156845/15.
DR
XX New antibody, antibody derivative or antigen-binding polypeptide that
PT inhibits proteolytic release of a soluble kidney injury molecule-1
PT polypeptide, useful for treating or preventing renal disease or injury,
PT e.g. renal cancer.
XX
XX Claim 4; Page 25; 43pp; English.
PS
XX The invention relates to a novel antibody, antibody derivative or antigen
CC -binding polypeptide that inhibits proteolytic release of a soluble
CC kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.
CC The antibody, antibody derivative or antigen-binding polypeptide is
CC useful for treating or preventing renal disease or injury, e.g. renal
CC cancer. The antibody is also useful for inhibiting shedding of the KIM-1
CC polypeptide. This sequence represents a human KIM-1 mucin domain related
CC peptide of the invention
XX
XX Sequence 18 AA;
  Query Match          36.0%; Score 99; DB 6; Length 18;
  Best Local Similarity 100.0%; Pred. No. 2.5e-05;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 16 SSDGLWNNNTQLFLEHS 33
  DB 1 SSDGLWNNNTQLFLEHS 18

RESULT 4
AAO26688
ID AAO26688 standard; peptide; 18 AA.
XX
XX AAO26688;
AC
XX
XX 20-MAR-2003 (first entry)
XX Human KIM-1 mucin domain related peptide, SEQ ID No 16.
DE
XX Cytostatic; gene therapy; antibody; antigen; antigen-binding;
KW proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;
KW renal disease; injury; renal cancer.
XX
XX Synthetic.
OS
XX WO200298920-A1.
PN
XX

```

PD 12-DEC-2002.
 XX
 PF 31-MAY-2002; 2002WO-US017402.
 XX
 PR 01-JUN-2001; 2001US-0295449P.
 PR 04-JUN-2001; 2001US-0295907P.
 XX
 XX (BIOJ) BIOGEN INC.
 PA (GHEO) GEN HOSPITAL CORP.
 XX
 PI Bailly V, Bonventre J;
 XX
 XX WPI; 2003-156845/15.
 DR
 XX New antibody, antibody derivative or antigen-binding polypeptide that
 PT inhibits proteolytic release of a soluble kidney injury molecule-1
 PT polypeptide, useful for treating or preventing renal disease or injury,
 PT e.g. renal cancer.
 XX
 XX Disclosure; Fig 1A; 42pp; English.
 PS
 XX The invention relates to a novel antibody, antibody derivative or antigen
 CC -binding polypeptide that inhibits proteolytic release of a soluble
 CC kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.
 CC The antibody, antibody derivative or antigen-binding polypeptide is
 CC useful for treating or preventing renal disease or injury, e.g. renal
 CC cancer. The antibody is also useful for inhibiting shedding of the KIM-1
 CC polypeptide. This sequence represents a human KIM-1 mucin domain related
 CC peptide of the invention
 XX
 SQ Sequence 18 AA;
 Query Match 29.8%; Score 82; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.0034;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PLYSYTTDGNDRVTE 15
 DB 4 PLYSYTTDGNDRVTE 18
 RESULT 6
 ADA98306
 ID ADA98306 standard; protein; 43 AA.
 XX
 AC ADA98306;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human secreted protein sequence #147.
 XX
 KW human; secreted protein; cardiovascular disorder; arrhythmia;
 KW atherosclerosis; stroke; endocarditis; congestive heart failure;
 KW rheumatic heart disease; cardiomyopathy; haemorrhoids; varicose veins;
 KW migraine; thrombosis; neural disorder; immune system disorder;
 KW muscular disorder; reproductive disorder; gastrointestinal disorder;
 KW pulmonary disorder; renal disorder; proliferative disorder; cancer.
 XX
 OS Homo sapiens.
 XX
 XX WO2003004623-A2.
 PN
 PD 16-JAN-2003.
 XX
 PF 26-MAR-2002; 2002WO-US009922.
 XX
 XX 27-MAR-2001; 2001US-0278650P.
 PR 12-SEP-2001; 2001US-00950082.
 PR 12-SEP-2001; 2001US-00950083.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Rosen CA, Ruben SM;
 PI
 XX WPI; 2003-247946/24.
 DR
 XX New human secreted polypeptide and nucleic acid molecules, useful for
 PT diagnosing, preventing, prognosticating or treating cardiovascular
 PT disorders (e.g. arrhythmia, atherosclerosis, cardiomyopathy, or
 PT thrombosis).
 XX
 XX Claim 1; SEQ ID NO 414; 1572pp; English.
 PS
 XX The invention comprises the amino acid and coding sequence of human
 CC secreted proteins. The DNA and protein sequences of the invention are
 CC useful in the treatment of cardiovascular disorders, such as: arrhythmia,
 CC atherosclerosis, stroke, endocarditis, congestive heart failure,

PD 12-DEC-2002.
 XX
 PF 31-MAY-2002; 2002WO-US017402.
 XX
 PR 01-JUN-2001; 2001US-0295449P.
 PR 04-JUN-2001; 2001US-0295907P.
 XX
 XX (BIOJ) BIOGEN INC.
 PA (GHEO) GEN HOSPITAL CORP.
 XX
 PI Bailly V, Bonventre J;
 XX
 XX WPI; 2003-156845/15.
 DR
 XX New antibody, antibody derivative or antigen-binding polypeptide that
 PT inhibits proteolytic release of a soluble kidney injury molecule-1
 PT polypeptide, useful for treating or preventing renal disease or injury,
 PT e.g. renal cancer.
 XX
 XX Disclosure; Fig 1A; 42pp; English.
 PS
 XX The invention relates to a novel antibody, antibody derivative or antigen
 CC -binding polypeptide that inhibits proteolytic release of a soluble
 CC kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.
 CC The antibody, antibody derivative or antigen-binding polypeptide is
 CC useful for treating or preventing renal disease or injury, e.g. renal
 CC cancer. The antibody is also useful for inhibiting shedding of the KIM-1
 CC polypeptide. This sequence represents a human KIM-1 mucin domain related
 CC peptide of the invention
 XX
 SQ Sequence 18 AA;
 Query Match 32.7%; Score 90; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.00034;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 25 QTQLFLEHSLTANTTKG 42
 DB 1 QTQLFLEHSLTANTTKG 18
 RESULT 5
 AA028685
 ID AA028685 standard; peptide; 18 AA.
 XX
 AC AA028685;
 XX
 DT 20-MAR-2003 (first entry)
 XX
 DE Human KIM-1 mucin domain related peptide, SEQ ID No 13.
 XX
 KW Cytostatic; gene therapy; antibody; antigen; antigen-binding;
 KW proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;
 KW renal disease; injury; renal cancer.
 XX
 OS Synthetic.
 XX
 XX WO200298920-A1.
 PN
 PD 12-DEC-2002.
 XX
 PF 31-MAY-2002; 2002WO-US017402.
 XX
 XX 01-JUN-2001; 2001US-0295449P.
 PR 04-JUN-2001; 2001US-0295907P.
 XX
 XX (BIOJ) BIOGEN INC.
 PA (GHEO) GEN HOSPITAL CORP.
 XX
 PI Bailly V, Bonventre J;
 XX
 XX WPI; 2003-156845/15.
 DR
 XX

CC rheumatic heart disease, cardiomyopathy, haemorrhoids, varicose veins,
CC migraine, or thrombosis. The DNA and protein sequences may also be used
CC for treating or preventing: neural disorders, immune system disorders,
CC muscular disorders, reproductive disorders, gastrointestinal disorders,
CC pulmonary disorders, renal disorders, proliferative disorders and/or
CC cancerous diseases. The present amino acid sequence represents a human
CC secreted protein of the invention. NOTE: The present sequence is shown on
CC the WIPO website.
XX
SQ Sequence 43 AA;

Query Match 17.8%; Score 49; DB 6; Length 43;
Best Local Similarity 42.4%; Pred. No. 1.3e+02;
Matches 14; Conservative 4; Mismatches 13; Indels 2; Gaps 1;

Qy 20 LWNNNQTLFLEHSLTANTTKGIYAGVCISVL 52
|| : | | | | : : ||| : |||
Db 3 LWKCGRTT--LRASLLMIFTSCSWLGVCLSVL 33

RESULT 7

ADA44132
ID ADA44132 standard; protein; 43 AA.

AC ADA44132;

XX 20-NOV-2003 (first entry)

DT Human secreted protein SEQ ID 324.

DE Gene therapy; human; Antidiabetic; Anorectic; Ophthalmological;
KW Neuroprotective; Cerebroprotective; Antianemic.

XX Homo sapiens.

OS WO2003000865-A2.

PN 03-JAN-2003.

XX 26-MAR-2002; 2002WO-US009105.

XX 27-MAR-2001; 2001US-0278650P.

PR 12-SEP-2001; 2001US-00950082.

PR 12-SEP-2001; 2001US-00950083.

XX (HUMA-) HUMAN GENOME SCI INC.

PA Rosen CA, Ruben SM;

PI WPI, 2003-184045/18.

DR N-FSDB; ADA43942.

XX A human secreted protein and nucleic acids useful for preparing a
PT diagnostic or pharmaceutical composition for diagnosing or treating
PT diabetes or conditions related to diabetes, e.g. hyperglycemia, obesity,
PT retinopathy, neuropathy.

XX Claim 1; SEQ ID NO 324; 701pp; English.

XX The invention relates to novel genes and their fragments which are useful
CC for preventing, treating or ameliorating medical conditions e.g. by
CC protein or gene therapy. The genes are isolated from a range of human
CC tissues disclosed in the specification. The nucleic acids and proteins
CC are useful in the diagnosis, treatment and prevention of conditions
CC related to diabetes, e.g. hyperglycaemia, obesity, retinopathy,
CC polynuropathy, atherosclerosis, anaemia, stroke, gangrene, impotence,
CC infection, cataract, renal disorders, or endocrine disorders. The present
CC sequence was used to illustrate the invention.

XX Sequence 43 AA;

Query Match 17.8%; Score 49; DB 6; Length 43;
Best Local Similarity 42.4%; Pred. No. 1.3e+02;

Matches 14; Conservative 4; Mismatches 13; Indels 2; Gaps 1;
Qy 20 LWNNNQTLFLEHSLTANTTKGIYAGVCISVL 52
|| : | | | | : : ||| : |||
Db 3 LWKCGRTT--LRASLLMIFTSCSWLGVCLSVL 33

RESULT 8

ADC20470
ID ADC20470 standard; protein; 43 AA.

XX ADC20470;

DT 18-DEC-2003 (first entry)

DE Human secreted protein - amino acid sequence #151.

XX gene therapy; human; secreted protein; haemopoietic disorder;
KW haematological disorder; anaemia; haemophilia; inflammatory disorder;
KW inflammatory bowel disease; Crohn's disease; neoplastic disease; cancer;
KW leukaemia; wound healing; epithelial cell proliferation disorder;
KW immune disorder; autoimmune disorder; asthmatic disorder;
KW cardiovascular disorder; atherosclerosis; myocarditis;
KW infectious disease; HIV; AIDS; endocrine disorder; diabetes;
KW gastrointestinal disorder; duodenal ulcer; gastroenteritis.

XX Homo sapiens.

OS WO200292787-A2.

PN 21-NOV-2002.

XX 26-MAR-2002; 2002WO-US009257.

XX 27-MAR-2001; 2001US-0278650P.

PR 12-SEP-2001; 2001US-00950082.

PR 12-SEP-2001; 2001US-00950083.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

PI WPI, 2003-129287/12.

XX New human secreted proteins and nucleic acid molecules, useful for
PT preparing a diagnostic or pharmaceutical composition for diagnosing,
PT preventing or treating hematopoietic or hematologic disorders, e.g.
PT anemia or hemophilia.

XX Claim 1; SEQ ID NO 424; 1512pp; English.

XX The invention comprises the amino acid and coding sequences of human
CC secreted proteins. The DNA and protein sequences of the invention are
CC useful for detecting, preventing, diagnosing, prognosticating, treating
CC or ameliorating: haematopoietic or haematological disorders (e.g. anaemia
CC and haemophilia); inflammatory disorders (e.g. inflammatory bowel disease
CC and Crohn's disease); neoplastic disease (e.g. cancer and leukaemia);
CC wound healing and disorders of epithelial cell proliferation; immune
CC disorders (e.g. autoimmune disorders and asthmatic disorders);
CC cardiovascular disorders (e.g. atherosclerosis and myocarditis);
CC infectious disease (e.g. HIV/AIDS); endocrine disorders (e.g. diabetes);
CC and gastrointestinal disorders (e.g. duodenal ulcers and
CC gastroenteritis). The present amino acid sequence represents a human
CC secreted protein of the invention.

XX Sequence 43 AA;

Query Match 17.8%; Score 49; DB 7; Length 43;
Best Local Similarity 42.4%; Pred. No. 1.3e+02;
Matches 14; Conservative 4; Mismatches 13; Indels 2; Gaps 1;

Qy 20 LWNNNQTLFLEHSLTANTTKGIYAGVCISVL 52
|| : | | | | : : ||| : |||


```

Db      3 LMKCGRTT--LRASLLMIFTSCSWMLGVCLSVL 33
RESULT 9
ADP10760
ID      ADF10760 standard; protein; 43 AA.
XX
AC      ADF10760;
XX
DT      12-FEB-2004 (first entry)
XX
DE      Human secreted protein #82.
XX
KW      H6EDM64; HBHAA05; HBJCR46; HCWXS51; HCQDH72; HDPQ30; HE2QM39;
KW      HE9EA10; HGBHP91; HLDQU79; Cytostatic; Hepatotropic; Antidiabetic;
KW      Antinflammatory; neuroprotective; Anti-HIV; Vulnery; Gynecological;
KW      Antinfertility; Gene therapy; gastrointestinal disorder; cancer;
KW      Alzheimer's disease; chromosome identification.
XX
OS      Homo sapiens.
XX
PN      WO200299085-A2.
XX
PD      12-DEC-2002.
XX
PF      26-MAR-2002; 2002WO-US009135.
XX
PR      27-MAR-2001; 2001US-0278650P.
PR      12-SEP-2001; 2001US-00950082.
PR      12-SEP-2001; 2001US-00950083.
XX
PA      (HUMA-) HUMAN GENOME SCI INC.
XX
PI      Rosen CA, Ruben SM;
XX
DR      WPI; 2003-221310/21.
XX
PT      New human secreted polypeptides for diagnosing and treating neural,
PT      immune system, muscular, reproductive, gastrointestinal, cardiovascular,
PT      renal, and proliferative disorders and cancerous diseases.
XX
PS      Claim 1; SEQ ID NO 223; 855pp; English.
XX
CC      The present invention relates to an isolated polypeptide chosen from 123
CC      human secreted proteins, such as, H6EDM64, HBHAA05, HBJCR46, HBKJDK16,
CC      HCWXS51, HCQDH72, HDPQ30, HE2QM39, HE9EA10, HGBHP91 and HLDQU79. The
CC      polypeptides are useful for the preparation of a diagnostic or
CC      pharmaceutical composition for diagnosing or and are useful for treating
CC      or preventing diseases or conditions, such as neural, immune system,
CC      muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC      renal, proliferative disorders and cancerous diseases and conditions. The
CC      polypeptides have immune activity, chemotactic activity, and binding
CC      activity. To treat and prevent neuronal damage which occurs in certain
CC      neuronal disorders or neuro-degenerative conditions such as Alzheimer's
CC      disease, Parkinson's disease, and acquired immunodeficiency syndrome
CC      (AIDS)-related complex, and to prevent skin aging due to sunburn by
CC      stimulating keratinocyte growth. The molecules are also useful to
CC      modulate mammalian characteristics including . The encoding sequences are
CC      useful for chromosome identification, radiation hybrid mapping, in gene
CC      therapy, for identifying individuals from minute biological samples, as
CC      additional DNA markers for restriction fragment length polymorphism
CC      (RFLP), in forensic biology, molecular weight markers on Southern gels,
CC      as diagnostic probes for the presence of a specific mRNA in a particular
CC      cell type, to raise anti-DNA antibodies using DNA immunization
CC      techniques, and as an antigen to elicit an immune response. The present
CC      sequence represents a human secreted protein of the invention.
XX
SQ      Sequence 43 AA;
XX
Query Match      17.8%; Score 49; DB 7; Length 43;
Best Local Similarity 42.4%; Pred. No. 1.3e+02;
Matches 14; Conservative 4; Mismatches 13; Indels 2; Gaps 1;

Db      3 LMKCGRTT--LRASLLMIFTSCSWMLGVCLSVL 33
RESULT 10
AAB29810
ID      AAB29810 standard; protein; 44 AA.
XX
AC      AAB29810;
XX
DT      09-FEB-2001 (first entry)
XX
DE      Human secreted protein SEQ ID NO: 68.
XX
KW      Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW      antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW      vulnery; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW      cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW      neurological disease; infection; human; secreted protein.
XX
OS      Homo sapiens.
XX
PN      WO2000061779-A1.
XX
PD      19-OCT-2000.
XX
PF      06-APR-2000; 2000WO-US009068.
XX
PR      09-APR-1999; 99US-0128699P.
PR      20-JAN-2000; 2000US-0177050P.
XX
PA      (HUMA-) HUMAN GENOME SCI INC.
XX
PI      Rosen CA, Ruben SM, Komatsoulis G;
XX
DR      WPI; 2000-647424/62.
XX
DR      N-PSDB; AAC63418.
XX
PT      Isolated nucleic acid molecule encoding a human secreted protein is used
PT      in preventing, treating or ameliorating a medical condition.
XX
PS      Claim 11; Page 431; 495pp; English.
XX
CC      Sequences AAB29802-B29850 represent the amino acid sequences of 49 human
CC      secreted proteins encoded by the genes AAC63410-C63458. The genes and
CC      proteins are useful for preventing, ameliorating or treating medical
CC      conditions, e.g. by protein or gene therapy. The genes are isolated from
CC      a range of human tissues disclosed in the specification. The nucleic
CC      acids, proteins, antibodies and (ant)agonists are useful in the
CC      diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC      ovarian cancer, and other cancers of the adrenal gland, bone, bone
CC      marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b)
CC      immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC      anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC      multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC      cardiovascular disorders such as myocardial ischaemia; (d) wound healing
CC      ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC      infectious diseases such as viral, bacterial, fungal and parasitic
CC      infections
XX
SQ      Sequence 44 AA;
XX
Query Match      17.8%; Score 49; DB 3; Length 44;
Best Local Similarity 42.4%; Pred. No. 1.4e+02;
Matches 14; Conservative 4; Mismatches 13; Indels 2; Gaps 1;

Db      3 LMKCGRTT--LRASLLMIFTSCSWMLGVCLSVL 33
RESULT 11
LWNNNOTQLFLEHSLLTANTTKGIYAGVCISVL 52
3 LMKCGRTT--LRASLLMIFTSCSWMLGVCLSVL 33
XX
Query Match      17.8%; Score 49; DB 3; Length 44;
Best Local Similarity 42.4%; Pred. No. 1.4e+02;
Matches 14; Conservative 4; Mismatches 13; Indels 2; Gaps 1;

```


DT 15-OCT-2003 (first entry)
 DE Bacteriophage Tuc2009 lys protein amino acids 332-375.
 XX
 XX Antibacterial; protozoacide; vaccine; cell-wall material; anchor protein;
 KW Gram-positive bacterium; Lactococcus lactis; Acma; biocatalyst;
 KW mucosal immunization; bioadsorbent; biofilter; microbiocatalyst;
 KW malaria; Streptococcus pneumoniae; fusion gene;
 KW Streptococcus pneumoniae; protease maturation protein.
 XX
 OS Bacteriophage Tuc2009.
 XX
 XX WO2002101026-A2.
 PN
 XX 19-DEC-2002.
 PD
 XX 11-JUN-2002; 2002WO-NL000383.
 PF
 XX 11-JUN-2001; 2001EP-00202239.
 PR
 XX (NANO-) APPLIED NANOSYSTEMS BV.
 PA
 XX Leenhouts CJ, Ramasamy R, Steen A, Kok J, Buist G, Kuipers OP;
 PI WPI; 2003-167404/16.
 DR
 XX Improving binding of a proteinaceous substance e.g. an AcmaA-type protein
 PT to a cell-wall material of microorganisms, comprises treating the
 PT material with a solution capable of removing protein or carbohydrate from
 PT the material.
 XX
 XX Example 3; Fig 24; 77pp; English.
 PS
 XX The invention relates to a method of obtaining cell-wall material of a
 CC Gram-positive bacterium with improved capacity for binding to a
 CC proteinaceous substance (PS), or binding PS to cell-wall material of the
 CC bacterium, by treating the cell-wall material with a solution capable of
 CC removing a cell-wall component such as a protein, (lipo)teichoic acid or
 CC carbohydrate from the material. The method especially uses the binding of
 CC the PS with an anchor protein from the cell wall of the organism. The
 CC anchor protein is preferably the Lactococcus lactis AcmaA cell wall
 CC binding domain or its homolog or functional derivative. The method is
 CC useful for improving binding of proteinaceous substance to cell wall
 CC material of gram-positive bacterium, e.g. for the preparation of a
 CC immunization and for preparing a biocatalyst. The preparation is also
 CC useful for generating bioadsorbents or biofilters for environmental
 CC purposes, microbiocatalysts and diagnostic tools. Also for vaccination
 CC Streptococcus pneumoniae. In an example of the invention, acid
 CC pretreatment of Gram-positive bacteria to enhance binding of AcmaA protein
 CC anchor fusion is investigated by the construction of a reporter plasmid
 CC encoding a fusion gene of the L. lactis AcmaA protein and the
 CC Streptococcus pneumoniae protease maturation protein PpmA. This sequence
 CC represents a homologue of the Lactococcus lactis AcmaA anchor protein. The
 CC region can be used in the generation of the fusion protein of the
 CC invention
 XX
 XX Sequence 44 AA;
 SQ

Query Match 17.1%; Score 47; DB 6; Length 44;
 Best Local Similarity 32.6%; Pred. No. 2.5e+02;
 Matches 15; Conservative 6; Mismatches 21; Indels 4; Gaps 2;
 QY 5 YTTDGNVTSSDGLWNNNQTLFLEHSLTANTTKGIYAGVCIS 50
 DB 1 YVVKQDTLSGIASN-WGTNWQELARQNSLSPNM---IYAGQVIS 42

RESULT 14
 ADF70020
 ID ADF70020 standard; protein; 44 AA.
 XX

AC ADF70020;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE AcmaA-type homologue amino acid sequence.
 XX
 XX delivery; targeting system; AcmaA-type anchor protein; solid tumour;
 KW health; medical; agricultural; cosmetic; controlled release.
 KW
 OS Unidentified.
 XX
 XX WO2003084508-A1.
 PN
 XX 16-OCT-2003.
 PD
 XX 04-APR-2003; 2003WO-NL000256.
 PF
 XX 04-APR-2002; 2002EP-00076316.
 PR
 XX 04-APR-2002; 2002US-0369927P.
 PR
 XX 05-APR-2002; 2002US-0370485P.
 PR
 XX 20-DEC-2002; 2002EP-00080481.
 PR
 XX (NANO-) APPLIED NANOSYSTEMS BV.
 PA
 XX Frieseen RHE, Leenhouts CJ, Hektor HJ, Van Esch JH, Heeres A;
 PI Robillard GT;
 PI
 XX WPI; 2003-877005/81.
 DR
 XX Vehicle for targeted delivery of therapeutic or diagnostic agents,
 PT includes protein anchor and system for inducing availability of the
 PT agent.
 PT
 XX Example 3; Page 193; 303pp; English.
 PS
 XX The present invention describes a vehicle (A) for delivering a substance
 CC (I) to a predetermined site, which comprises (I); a system for inducing
 CC availability of at least one compartment of (A) towards the exterior;
 CC and, as targeting system for directing (A) to the site, an AcmaA-type
 CC anchor protein (II). (A) are used for delivery of diagnostic and
 CC therapeutic agents to predetermined sites in the body, particularly
 CC joints or solid tumours but can be used more generally for health,
 CC medical, agricultural and cosmetic applications. (A) significantly
 CC increases the half-life of peptides in the circulation and, by providing
 CC controlled release, ensures relatively high bioavailability, allowing
 CC therapeutic use of agents that would otherwise be too toxic for systemic
 CC administration. The native AcmaA peptide targets Gram-positive bacteria
 CC but its homologues can be engineered to have different selectivity. The
 CC present sequence is used in the exemplification of the present invention.
 XX
 XX Sequence 44 AA;
 SQ

Query Match 17.1%; Score 47; DB 7; Length 44;
 Best Local Similarity 32.6%; Pred. No. 2.5e+02;
 Matches 15; Conservative 6; Mismatches 21; Indels 4; Gaps 2;
 QY 5 YTTDGNVTSSDGLWNNNQTLFLEHSLTANTTKGIYAGVCIS 50
 DB 1 YVVKQDTLSGIASN-WGTNWQELARQNSLSPNM---IYAGQVIS 42

RESULT 15
 AAM92081
 ID AAM92081 standard; protein; 49 AA.
 XX
 AC AAM92081;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 XX Human digestive system antigen SEQ ID NO: 1430.
 DE
 XX Human; digestive system antigen; gene therapy; cancer; appendicitis;
 KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
 KW

KW digestive system disorder; Meckel's diverticulum.

XX Homo sapiens.

PN WO20015314-A2.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US001324.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190078P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225757P.

PR 14-AUG-2000; 2000US-0225758P.

PR 14-AUG-2000; 2000US-0225759P.

PR 18-AUG-2000; 2000US-0226279P.

PR 22-AUG-2000; 2000US-0226681P.

PR 22-AUG-2000; 2000US-0226868P.

PR 22-AUG-2000; 2000US-0227182P.

PR 25-SEP-2000; 2000US-0234988P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241826P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-02559678P.

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Job time : 36.5521 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 08:57:16 ; Search time 20.8409 Seconds
(without alignments)
1277.688 Million cell updates/sec

Title: US-10-718-321-7_COPY_249_300

Perfect score: 275

Sequence: 1 PLYSYTDCNDVTSSDGL.....SLLTANTTKGIYAGVCISVL 52

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	275	100.0	359	2	O43656	O43656 homo sapien
2	275	100.0	364	2	Q96D42	Q96D42 homo sapien
3	228	82.9	451	2	Q95144	Q95144 cercopithec
4	228	82.9	460	2	O18984	O18984 cercopithec
5	228	82.9	469	2	Q7JJ48	Q7JJ48 cercopithec
6	228	82.9	473	2	Q7JJ47	Q7JJ47 cercopithec
7	228	82.9	474	2	O46597	O46597 cercopithec
8	228	82.9	478	2	O46598	O46598 cercopithec
9	79	28.7	305	2	Q8VIM2	Q8VIM2 mus musculu
10	78	28.4	307	2	O54947	O54947 rattus norv
11	76.5	27.8	282	2	O8VIM1	O8VIM1 mus musculu
12	76.5	27.8	282	2	Q7TPU2	Q7TPU2 mus musculu
13	68	24.7	549	2	Q53969	Q53969 shigella dy
14	67.5	24.5	460	2	Q7URM5	Q7URM5 rhodopirell
15	65	23.6	554	2	Q842D0	Q842D0 escherichia
16	65	23.6	554	2	Q9KJA0	Q9KJA0 escherichia
17	63	22.9	1687	2	Q7QIM9	Q7QIM9 anopheles g
18	62.5	22.7	639	1	YHR7_YEAST	YHR7_YEAST
19	62.5	22.7	931	2	Q6WP59	Q6WP59 dengue viru
20	62.5	22.7	931	2	Q6WP60	Q6WP60 dengue viru
21	62.5	22.7	931	2	Q6WP63	Q6WP63 dengue viru
22	62.5	22.7	931	2	Q6WP68	Q6WP68 dengue viru
23	62.5	22.7	931	2	Q6WP69	Q6WP69 dengue viru
24	62.5	22.7	931	2	Q6WP70	Q6WP70 dengue viru
25	62.5	22.7	1269	2	Q97206	Q97206 sulfolobus
26	62.5	22.7	3392	2	Q8JQD9	Q8JQD9 dengue viru
27	62.5	22.7	3392	2	Q91NH1	Q91NH1 dengue viru
28	62.5	22.7	3392	2	Q6WP58	Q6WP58 dengue viru
29	62.5	22.7	3392	2	Q80KC7	Q80KC7 dengue viru
30	62	22.5	329	1	SRAC_CABEEL	Q09208 caenorhabdi
31	62	22.5	411	2	Q23351	Q23351 caenorhabdi

32	62	22.5	472	1	VL2_HPV34	P36758 human papil
33	62	22.5	842	2	Q9U0J9	Q9U0J9 plasmodium
34	61	22.2	133	2	Q6GZ26	Q6GZ26 fremyella d
35	61	22.2	1255	2	O36287	O36287 venezuelan
36	60.5	22.0	103	1	CYC_THUAA	P81459 thunnus ala
37	60.5	22.0	126	2	Q9P819	Q9P819 erwinia amy
38	60.5	22.0	474	2	Q9H751	Q9H751 homo sapien
39	60.5	22.0	474	2	Q9HC44	Q9HC44 homo sapien
40	60.5	22.0	3056	2	Q7USQ0	Q7USQ0 rhodopirell
41	60	21.8	282	2	Q7RJE4	Q7RJE4 plasmodium
42	60	21.8	287	2	O52953	O52953 bacillus su
43	60	21.8	338	2	Q9SQ06	Q9SQ06 arabidopsis
44	60	21.8	602	1	NRGI_CHICK	Q05199 gallus gall
45	60	21.8	1850	2	Q75CI2	Q75CI2 ashbya goss

ALIGNMENTS

RESULT 1

O43656 PRELIMINARY; PRT; 359 AA.

AC O43656; (Tremblrel. 06, Created)

DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)

DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)

DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)

DE Hepatitis A virus cellular receptor 1.

GN Name=HAVcr-1;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=98325180; PubMed=9658108;

RA Feigelsstock D., Thompson P., Mattoo P., Zhang Y., Kaplan G.G.;

RT "The human homolog of HAVcr-1 codes for a hepatitis A virus cellular receptor.";

RL J. Virol. 72:6621-6628(1998).

DR EMBL; AF043724; RAC39862.1; -.

DR GO; GO:0004872; Fireceptor activity; IEA.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003006; IG_MHC.

DR SMART; SM00409; IG_1.

DR PROSITE; PS00835; IG_LIKE; 1.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

KW Receptor.

SQ SEQUENCE 359 AA; 38704 MW; C207FEC562DC62CA CRC64;

Query Match 100.0%; Score 275; DB 2; Length 359;

Best Local Similarity 100.0%; Pred. No. 3e-25; 0; Gaps 0;

Matches 52; Conservative 0; Mismatches 0; Indels 0;

QY 1 PLYSYTDCNDVTSSDGLWNNNQQLFLEHSLLTANTTKGIYAGVCISVL 52
|||||

DB 249 PLYSYTDCNDVTSSDGLWNNNQQLFLEHSLLTANTTKGIYAGVCISVL 300
|||||

RESULT 2

Q96D42 PRELIMINARY; PRT; 364 AA.

AC Q96D42; (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)

DE HAVCR1 protein.

GN Name=HAVCR1;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

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RN RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.B., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalke U., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN RP SEQUENCE FROM N.A.
RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC03325; AAH3325.1; -.
DR EMBL; CR457114; CAG33395.1; -.
DR Genew; HGNC:17866; HAVCR1.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 364 AA; 39249 MW; AA67C7DC7FAC81F1 CRC64;

Query Match 100.0%; Score 275; DB 2; Length 364;
Best Local Similarity 100.0%; Pred. No. 3e-25; Mismatches 0; Indels 0; Gaps 0;
Matches 52; Conservative 0;

QY 1 PLYSYTTDGNQDVTVESSDGLMNNNTQLFLEHSLLTANTTKGIYAGVCISVL 52
DB 254 PLYSYTTDGNQDVTVESSDGLMNNNTQLFLEHSLLTANTTKGIYAGVCISVL 305

RESULT 3
Q95144 PRELIMINARY; PRT; 451 AA.
AC Q95144;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE HAVCR-1 protein precursor.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=97015129; PubMed=8861957;
RA Kaplan G., Totsuka A., Thompson P., Akateuka T., Moritsugu Y.,
RA Feinstein S.M.;
RT "Identification of a surface glycoprotein on African green monkey

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RT kidney cells as a receptor for hepatitis A virus.";
RL EMBL; J. 15:4282-4296(1996).
DR PIR; S71754; S71754.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Signal.
FT SIGNAL 1 17 Potential.
SQ SEQUENCE 451 AA; 48774 MW; SD395C5455AA4332 CRC64;

Query Match 82.9%; Score 228; DB 2; Length 451;
Best Local Similarity 84.6%; Pred. No. 2.2e-19;
Matches 44; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 PLYSYTTDGNQDVTVESSDGLMNNNTQLFLEHSLLTANTTKGIYAGVCISVL 52
DB 329 PLYSYTTDGNQDVTVESSDGLMNNNTQLFLEHSLLTANTTKGIYAGVCISVL 380

RESULT 4
O18984 PRELIMINARY; PRT; 460 AA.
AC O18984;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hepatitis A virus receptor.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN RP SEQUENCE FROM N.A.
RX MEDLINE=97368416; PubMed=9225030;
RA Ashida M., Hamada C.;
RT "Molecular cloning of the hepatitis A virus receptor from a simian
RT cell line.";
RL J. Gen. Virol. 78:1565-1569(1997).
DR EMBL; D88585; BAA21556.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 460 AA; 49687 MW; 1D1A0C1D832139EA CRC64;

Query Match 82.9%; Score 228; DB 2; Length 460;
Best Local Similarity 84.6%; Pred. No. 2.3e-19;
Matches 44; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 PLYSYTTDGNQDVTVESSDGLMNNNTQLFLEHSLLTANTTKGIYAGVCISVL 52
DB 338 PLYSYTTDGNQDVTVESSDGLMNNNTQLFLEHSLLTANTTKGIYAGVCISVL 389

RESULT 5
Q7JJ48 PRELIMINARY; PRT; 469 AA.
AC Q7JJ48;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hepatitis A virus cellular receptor 1 short form.
GN Name=HAVCr-1;
OS Cercopithecus aethiops (Green monkey) (Grivet).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecius.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98285791; PubMed=9621093;
RA Feigelsstock D., Thompson P., Mattoo P., Kaplan G.G.;
RT "Polymorphisms of the hepatitis A virus cellular receptor 1 in African
RT green monkey kidney cells result in antigenic variants that do not
RT react with protective monoclonal antibody 190/4."
RL J. Virol. 72:6218-6222(1998).
DR EMBL; AF043446; AAC39771.1; -.
DR GO; GO:0004872; Fireceptor activity; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 469 AA; 50561 MW; 27E386F47948F528 CRC64;

Query Match 82.9%; Score 228; DB 2; Length 469;
Best Local Similarity 84.6%; Pred. No. 2.4e-19;
Matches 44; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 PLYSYTTDGNVTSSDGLWNNQTLFLEHSLTANTTKGIYAGVCISVL 52
Db 347 PLYSYTTDGS DVTSSDGLWNNQTLSPHSQPMVNTTEGIYAGVCISVL 398

RESULT 6
Q7JJ47 PRELIMINARY; PRT; 473 AA.
ID Q7JJ47
AC Q7JJ47
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hepatitis A virus cellular receptor 1 short form.
GN Name=HAVcr-1;
OS Cercopithecius aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecius.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98285791; PubMed=9621093;
RA Feigelsstock D., Thompson P., Mattoo P., Kaplan G.G.;
RT "Polymorphisms of the hepatitis A virus cellular receptor 1 in African
RT green monkey kidney cells result in antigenic variants that do not
RT react with protective monoclonal antibody 190/4."
RL J. Virol. 72:6218-6222(1998).
DR EMBL; AF043448; AAC39773.1; -.
DR GO; GO:0004872; Fireceptor activity; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 473 AA; 50973 MW; CD15EF5EE79C8013 CRC64;

Query Match 82.9%; Score 228; DB 2; Length 473;
Best Local Similarity 84.6%; Pred. No. 2.4e-19;
Matches 44; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 PLYSYTTDGNVTSSDGLWNNQTLFLEHSLTANTTKGIYAGVCISVL 52
Db 351 PLYSYTTDGS DVTSSDGLWNNQTLSPHSQPMVNTTEGIYAGVCISVL 402

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RESULT 7
O46597 PRELIMINARY; PRT; 474 AA.
ID O46597
AC O46597
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hepatitis A virus cellular receptor 1 long form.
GN Name=HAVcr-1;
OS Cercopithecius aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecius.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98285791; PubMed=9621093;
RA Feigelsstock D., Thompson P., Mattoo P., Kaplan G.G.;
RT "Polymorphisms of the hepatitis A virus cellular receptor 1 in African
RT green monkey kidney cells result in antigenic variants that do not
RT react with protective monoclonal antibody 190/4."
RL J. Virol. 72:6218-6222(1998).
DR EMBL; AF043447; AAC39772.1; -.
DR GO; GO:0004872; Fireceptor activity; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 474 AA; 51088 MW; 472DF987CA220524 CRC64;

Query Match 82.9%; Score 228; DB 2; Length 474;
Best Local Similarity 84.6%; Pred. No. 2.4e-19;
Matches 44; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 PLYSYTTDGNVTSSDGLWNNQTLFLEHSLTANTTKGIYAGVCISVL 52
Db 352 PLYSYTTDGS DVTSSDGLWNNQTLSPHSQPMVNTTEGIYAGVCISVL 403

RESULT 8
O46598 PRELIMINARY; PRT; 478 AA.
ID O46598
AC O46598
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hepatitis A virus cellular receptor 1 long form.
GN Name=HAVcr-1;
OS Cercopithecius aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecius.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98285791; PubMed=9621093;
RA Feigelsstock D., Thompson P., Mattoo P., Kaplan G.G.;
RT "Polymorphisms of the hepatitis A virus cellular receptor 1 in African
RT green monkey kidney cells result in antigenic variants that do not
RT react with protective monoclonal antibody 190/4."
RL J. Virol. 72:6218-6222(1998).
DR EMBL; AF043449; AAC39774.1; -.
DR GO; GO:0004872; Fireceptor activity; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

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KW Receptor.
SQ SEQUENCE 478 AA; 51501 MW; 3A919655C752FF60 CRC64;

Query Match
Best Local Similarity 82.9%; Score 228; DB 2; Length 478;
Matches 44; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 PLYSYTDTGNDVTVTSSDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 52
DB 356 PLYSYTDTGNDVTVTSSDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 407

RESULT 9
Q8VIM2 PRELIMINARY; PRT; 305 AA.
AC Q8VIM2;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE TIM1.
GN Name=Havcr1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/c; TISSUE=Spleen;
RX MEDLINE=21582130; PubMed=11725301;
RA McIntire J.J., Umetsu S.E., Akbari O., Potter M., Kuchroo V.K.,
RA Barsh G.S., Freeman G.J., Umetsu D.T., DeKruyff R.H.;
RT "Identification of Tapr (an airway hyperreactivity regulatory locus)
RT and the linked Tim gene family.";
RL Nat. Immunol. 2:1109-1116(2001).
DR EMBL; AF399829; AAL35774.1; -.
DR MGD; MGI:2159680; Havcr1.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR SEQUENCE 305 AA; 33391 MW; 8F4EA38627FE85FB CRC64;

Query Match
Best Local Similarity 42.0%; Score 79; DB 2; Length 305;
Matches 21; Conservative 6; Mismatches 19; Indels 4; Gaps 3;

QY 4 SYT-TDGNVTVTSSDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 52
DB 201 SHTPTDNGTGTSSGD-TWSNHTA--IPPQKPKQKPTKGFYVGICIAAL 247

RESULT 10
O54947 PRELIMINARY; PRT; 307 AA.
AC O54947;
DT 01-JUN-1998 (TRENBLrel. 06, Created)
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Kidney injury molecule-1 (KIM-1 protein).
GN Name=KIM-1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
RX MEDLINE=98129827; PubMed=9461608; DOI=10.1074/jbc.273.7.4135;
RA Ichimura T., Bonventre J.V., Bailly V., Wei H., Hession C.A.,
RA Cate R.L., Sanicola M.;
RT "Kidney injury molecule-1 (KIM-1), a putative epithelial cell adhesion
RT molecule containing a novel immunoglobulin domain, is up-regulated in
RT renal cells after injury.";
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J. Biol. Chem. 273:4135-4142(1998).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF035963; AAC53546.1; -.
DR EMBL; BC061820; AAH61820.1; -.
DR InterPro; IPR003599; IG.
DR SMART; SM007110; IG-like.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR SEQUENCE 307 AA; 33963 MW; 736D1DD1F1549760 CRC64;

Query Match
Best Local Similarity 28.4%; Score 78; DB 2; Length 307;
Matches 21; Conservative 7; Mismatches 18; Indels 4; Gaps 3;

QY 4 SYT-TDGNVTVTSSDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 52
DB 199 SYTADWNGTGT-SSEAWNNHTVRIPLRKP--QRNPTKGFYVGMSVAAL 245

RESULT 11
Q8VIM1 PRELIMINARY; PRT; 282 AA.
AC Q8VIM1;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE TIM1.
GN Name=Havcr1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2; TISSUE=Spleen;
RX MEDLINE=21582130; PubMed=11725301;
RA McIntire J.J., Umetsu S.E., Akbari O., Potter M., Kuchroo V.K.,
RA Barsh G.S., Freeman G.J., Umetsu D.T., DeKruyff R.H.;
RT "Identification of Tapr (an airway hyperreactivity regulatory locus)
RT and the linked Tim gene family.";
RL Nat. Immunol. 2:1109-1116(2001).
DR EMBL; AF399830; AAL35775.1; -.
DR MGD; MGI:2159680; Havcr1.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
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DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
SQ SEQUENCE 282 AA; 30968 MW; 7D30E0698F0AC5F CRC64;

Query Match
Best Local Similarity 27.8%; Score 76.5; DB 2; Length 282;
Matches 18; Conservative 8; Mismatches 21; Indels 3; Gaps 2;

QY 3 YSYTTDGDNDTVTSSDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 52
   :::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 178 WTHKPDWNGTVTSSGD-TWSNHTA--IPPGKPKQXPKTKGFVVGICIAAL 224

RESULT 12
Q7TPU2 PRELIMINARY; PRT; 282 AA.
AC Q7TPU2
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Blasocyst;
EX MEDLINE=23288257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Roshtykli S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Blasocyst;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053400; AAH53400.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Hypothetical protein.
SQ SEQUENCE 282 AA; 30938 MW; 6D31E2778480AC5F CRC64;

Query Match
Best Local Similarity 27.8%; Score 76.5; DB 2; Length 282;
Matches 18; Conservative 8; Mismatches 21; Indels 3; Gaps 2;

QY 3 YSYTTDGDNDTVTSSDGLWNNQTLFLEHSLLTANTTKGIYAGVCISVL 52
   :::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 178 WTHKPDWNGTVTSSGD-TWSNHTA--IPPGKPKQXPKTKGFVVGICIAAL 224

RESULT 13
Q53969 PRELIMINARY; PRT; 549 AA.
AC Q53969
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Flagellin.
GN Name=flhC-SD;
OS Shigella dysenteriae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=622;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sh16;
RA Mahmoud M.A., Tominaga A., Abu Amar A.M., Enomoto M.;
RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; D26166; BAA05153.1; -.
DR HSP; P06179; IUCU.
DR GO; GO:0009420; C:flagellar filament (sensu Bacteria); IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0001539; P:ciliary or flagellar motility; IEA.
DR InterPro; IPR001029; Flagellin_C.
DR InterPro; IPR001492; Flagellin_N.
DR Pfam; PF00700; Flagellin_C; 1.
DR Pfam; PF00669; Flagellin_N; 1.
DR PRINTS; PR00207; FLAGELLIN.
DR ProDom; PD000316; Flagellin_C; 1.
KW Flagellum.
SQ SEQUENCE 549 AA; 57591 MW; 8C8A56DC661CB732 CRC64;

Query Match
Best Local Similarity 24.7%; Score 68; DB 2; Length 549;
Matches 21; Conservative 7; Mismatches 18; Indels 4; Gaps 2;

QY 4 SYTTDGDNDTVTSSDGLW--NNQTLFLEHSLLTANTTKGIYAGVCISV 51
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 322 SKTNAGTQAKLSLMANNANAKVITIDKGTFTANTIK--FDGVDISV 369

RESULT 14
Q7UKM5 PRELIMINARY; PRT; 460 AA.
AC Q7UKM5
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Similar to Cap5J protein-putative transmembrane protein.
GN Ordered locus names=RH10055;
OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; BX294150; CAD76607.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR007016; Wzy_C.
DR Pfam; PF04932; Wzy_C; 1.
KW Complete proteome; Transmembrane.
SQ SEQUENCE 460 AA; 48823 MW; CB4F7122CE5A7E1B CRC64;

Query Match
Best Local Similarity 24.5%; Score 67.5; DB 2; Length 460;
Matches 17; Conservative 5; Mismatches 10; Indels 7; Gaps 2;
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 08:57:16 ; Search time 57.6071-Seconds
(without alignments)
543.815 Million cell updates/sec

Title: US-10-718-321-6

Perfect score: 432
Sequence: 1 MFLPRQNHPEVATSPSPQP.....NNOTQFLFLESLLTANTTKG 81

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	432	100.0	81	6	AAO26678 Human KIM
2	432	100.0	298	8	ADQ76693 Human KIM
3	432	100.0	334	2	AAW38336 Human kid
4	432	100.0	334	6	AAO26679 KIM-1 rel
5	432	100.0	334	8	ADQ76696 Human kid
6	432	100.0	339	7	ADE36618 Plasmid p
7	432	100.0	339	7	ADE36592 Human NOV
8	432	100.0	359	6	ABR58582 Human can
9	432	100.0	359	6	ABP70439 Amino aci
10	432	100.0	359	6	ABP70438 Amino aci
11	432	100.0	359	6	ABR48174 Human bla
12	432	100.0	359	6	AAO26680 KIM-1 rel
13	432	100.0	359	7	ADE36594 Human NOV
14	432	100.0	359	7	ADN38984 Cancer/an
15	432	100.0	359	8	ADQ76690 Human kid
16	432	100.0	364	6	ABP70442 Amino aci
17	432	100.0	365	6	ABP70440 Amino aci
18	432	100.0	518	8	ADQ76691 Human KIM
19	427	98.8	364	6	ABP70443 Amino aci
20	423	97.9	359	6	ABP70441 Amino aci
21	396	91.7	263	7	ADE36629 Human NOV
22	396	91.7	263	7	ADE36622 Plasmid p
23	396	91.7	263	7	ADE36596 Human NOV
24	348	80.6	451	2	AAR92803 Hepatitis
25	101	23.4	18	6	AAO26686 Human KIM

26	99	22.9	18	6	AAO26687	Aao26687 Human KIM
27	99	22.9	18	6	AAO26673	Aao26673 Monoclonal
28	98	22.7	18	6	AAO26681	Aao26681 Human KIM
29	97	22.5	18	6	AAO26682	Aao26682 Human KIM
30	96	22.2	18	6	AAO26683	Aao26683 Human KIM
31	95	22.0	18	6	AAO26685	Aao26685 Human KIM
32	92	21.3	18	6	AAO26684	Aao26684 Human KIM
33	90	20.8	18	6	AAO26688	Aao26688 Human KIM
34	89	20.6	307	2	AAW38334	Aaw38334 Rat kidne
35	88	20.4	153	3	AAB42784	Aab42784 Human ORF
36	88	20.4	153	5	ABP69679	Abp69679 Human pol
37	79	18.3	681	5	ABB93650	Abb93650 Herbicida
38	76.5	17.7	282	6	ABP70431	Abp70431 Amino aci
39	76	17.6	447	3	AAB42121	Aab42121 Human ORF
40	76	17.6	647	3	AAV53000	Aav53000 Human sec
41	76	17.6	893	7	ADK40920	Adk40920 Novel hum
42	76	17.6	893	8	ADR15641	Adr15641 Kinase 42
43	75	17.4	8360	6	AAE35499	Aae35499 Streptomy
44	74.5	17.2	539	6	ABP78670	Abp78670 N. gonorr
45	72.5	16.8	219	3	AAG19395	Aag19395 Arabidops

ALIGNMENTS

RESULT 1
AAO26678
ID AAO26678 standard; protein; 81 AA.
XX
AC AAO26678;
XX
DT 20-MAR-2003 (first entry)
XX
DE Human KIM-1 mucin domain protein, SEQ ID No 6.
XX
KW Cytostatic; gene therapy; antibody; antigen; antigen-binding;
KW proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;
KW renal disease; injury; renal cancer; human.
XX
OS Homo sapiens.
XX
PN WO200298920-A1.
XX
PD 12-DEC-2002.
XX
PF 31-MAY-2002; 2002WO-US017402.
XX
PR 01-JUN-2001; 2001US-0295449P.
PR 04-JUN-2001; 2001US-0295907P.
XX
(BIOJ) BIOGEN INC.
(GEHO) GEN HOSPITAL CORP.
XX
PI Bailly V, Bonventre J;
XX
DR WPI; 2003-156845/15.
XX
PT New antibody, antibody derivative or antigen-binding polypeptide that
PT inhibits proteolytic release of a soluble kidney injury molecule-1
PT polypeptide, useful for treating or preventing renal disease or injury,
e.g. renal cancer.
XX
PS Disclosure; Fig 1A; 42pp; English.
XX
CC The invention relates to a novel antibody, antibody derivative or antigen
CC -binding polypeptide that inhibits proteolytic release of a soluble
CC kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.
CC The antibody, antibody derivative or antigen-binding polypeptide is
CC useful for treating or preventing renal disease or injury, e.g. renal
CC cancer. The antibody is also useful for inhibiting shedding of the KIM-1
CC polypeptide. This sequence represents a human KIM-1 mucin domain protein
CC of the invention
XX

SQ Sequence 81 AA;
 Query Match 100.0%; Score 432; DB 6; Length 81;
 Best Local Similarity 100.0%; Pred. No. 1.7e-36;
 Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPLPRQNHVPVATSPSPQPAETHPTTLOGAIRREPTSSPLSYTTDGNDDVTSSDGLW 60
 DB 1 MPLPRQNHVPVATSPSPQPAETHPTTLOGAIRREPTSSPLSYTTDGNDDVTSSDGLW 60

QY 61 NNNQTLFLEHSLLTANTTKG 81
 DB 61 NNNQTLFLEHSLLTANTTKG 81

RESULT 2
 ADQ76693
 ID ADQ76693 standard; protein; 298 AA.
 XX
 AC ADQ76693;
 XX
 DT 07-OCT-2004 (first entry)
 XX Human KIM-1 extracellular domain-6xHis fusion.
 DE
 XX Human; KIM-1; kidney injury module-1; immunosuppressive; protozoasides;
 KW muscular-gen.; neuroprotective; antianaemic; antithyroid; haemostatic;
 KW antiallergic; antiinflammatory; vasotropic; nephropic.
 XX
 OS Homo sapiens.
 OS Synthetic.

Key Location/Qualifiers
 Peptide 1..20
 /label= Signal_peptide
 WO2004060041-A2.
 22-JUL-2004.
 29-DEC-2003; 2003WO-US041294.
 30-DEC-2002; 2002US-0436934P.
 (BIOG-) BIOGEN IDEC MA INC.
 Rennett PD;
 WPI; 2004-534277/51.

Use of a kidney injury molecule-1 (KIM-1) antagonist for e.g. treating Th2 cell-mediated diseases or inflammatory diseases, inhibiting B cell activation, or inhibiting production of a subset of antibodies against one or more antigens.

Example 3; Page 33; 68pp; English.

The present sequence is that of a polypeptide comprising the extracellular domain (residues 1-290) of human kidney injury molecule-1 (KIM-1) ADQ76690 fused to a C-terminal 6xHis tag peptide. A plasmid comprising DNA encoding this sequence under control of a CMV promoter was used for transient constitutive expression of the polypeptide in mammalian cells in an example from the invention. The invention provides methods for therapeutically modulating immune function in autoimmune diseases and other disorders of the mammalian immune system. A method is claimed for inhibiting signalling between a T cell and a second cell, e.g. an antigen-presenting cell, in a mammal. The method involves identifying a mammal with an immune disease or disorder, or one preparing to receive a tissue graft, and administering a KIM-1 antagonist, especially a polypeptide comprising: a KIM-1 Ig domain, and lacking a transmembrane domain and a KIM-1 cytoplasmic domain; an anti-KIM-1 antibody; or an antigen-binding fragment of an anti-KIM-1 antibody. Preferably, the KIM-1 antagonist is a soluble polypeptide, which can

CC include a KIM-1 mucin domain in addition to the KIM Ig domain, and may include a heterologous moiety such as an Fc moiety. The antagonist may be conjugated to a polymer such as polyethylene glycol. The KIM-1 antagonist is used in methods of: inhibiting activation of a B cell in a mammal; inhibiting disease relapse in an autoimmune disease; inhibiting epitope spreading in an autoimmune disease; treating a Th2 cell-mediated disease (e.g. myasthenia gravis, autoimmune haemolytic anaemia, Chagas disease, Grave's disease, idiopathic thrombocytopenia purpura, Wegener's granulomatosis, polyarteritis nodosa, rapidly progressive crescentic glomerulonephritis, graft-versus-host disease, or systemic lupus nephritis) or inflammatory disease or disorder (e.g. inflammatory bowel diseases such as Crohn's disease, ulcerative colitis, and ileitis); and inhibiting secretion of IFN-gamma by lymphocytes.

SQ Sequence 298 AA;
 Query Match 100.0%; Score 432; DB 8; Length 298;
 Best Local Similarity 100.0%; Pred. No. 8.1e-36;
 Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPLPRQNHVPVATSPSPQPAETHPTTLOGAIRREPTSSPLSYTTDGNDDVTSSDGLW 60
 DB 210 MPLPRQNHVPVATSPSPQPAETHPTTLOGAIRREPTSSPLSYTTDGNDDVTSSDGLW 269

QY 61 NNNQTLFLEHSLLTANTTKG 81
 DB 270 NNNQTLFLEHSLLTANTTKG 290

RESULT 3
 AA38336
 ID AA38336 standard; protein; 334 AA.
 XX
 AC AA38336;
 XX
 DT 21-MAY-1998 (first entry)
 XX Human kidney injury related molecule (KIM).
 DE
 XX Kidney injury related molecule; KIM; human; renal disease; injury;
 KW nephritis; tissue regeneration; therapy; monoclonal antibody.
 XX
 OS Homo sapiens.
 XX
 PN WO9744460-A1.
 XX
 PD 27-NOV-1997.
 XX
 PF 23-MAY-1997; 97WO-US009303.
 XX
 PR 24-MAY-1996; 96US-0018228P.
 PR 23-AUG-1996; 96US-0023442P.
 XX
 PA (BIOJ) BIOGEN INC.
 XX
 PI Sanicola-Nadel M, Bonventre JV, Hession CA, Ichimura T, Wei H;
 PI Cate RL;
 XX
 DR WPI; 1998-018514/02.
 XX
 PT DNA encoding kidney injury related molecule - which is upregulated in injured or regenerating tissue, useful to promote growth of new tissue and survival of damaged tissue.
 PT
 XX Claim 9; Page 46-47; 68pp; English.
 PS
 CC This protein, designated kidney injury related molecule (KIM), is up-regulated in injured or regenerating tissue. Its amino acid sequence was deduced from a clone (see AAW96035) obtained from a human embryonic liver library. A 572-amino acid (see AAW38335) and a 307-amino acid rat KIM (see AAW38334) are also claimed. Recombinant KIM polypeptides can be expressed in prokaryotic and eukaryotic host cells using a claimed process. Soluble variants fused to a toxin, imageable compound or

CC radionuclide, and IgG fusion proteins are also claimed. KIM, or an
CC agonist, can be used to treat renal disease and to promote the growth of new
CC tissue or the survival of damaged tissue, generally in conditions where
CC the binding of specific ligand to KIM stimulates cell growth, maintains
CC cellular differentiation or reduces apoptosis, e.g. in cases of renal
CC failure, nephritis, kidney transplants, toxic or hypoxic injury. A
CC monoclonal antibody specific for KIM can be used to treat renal disease,
CC e.g. where binding of KIM to ligand results in neoplasia, loss of
CC cellular function, susceptibility to apoptosis or promotion of
CC inflammation, deliver imaging agents to KIM expressing cells in vivo or
CC in vitro and measure KIM concentration by immunoassay.
CC Damage/regeneration of renal cells can be determined by measuring KIM,
CC particularly to diagnose or monitor the progress of disease or therapy.
CC KIM-expressing tumour cells can be inhibited by treatment with a fusion
CC protein comprising KIM ligand or MAb with a toxin or radionuclide, and
CC tumour cells that express KIM ligand can be inhibited with similarly
CC tagged KIM or anti-KIM ligand antibody
XX
SQ Sequence 334 AA;

Query Match 100.0%; Score 432; DB 2; Length 334;
Best Local Similarity 100.0%; Pred. No. 9.3e-36;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPLPRQHPEVATSPSSPOPAETHPTTLQGAIRREPTSSPLSYTTDGNVTVESDGLW 60
DB 210 MPLPRQHPEVATSPSSPOPAETHPTTLQGAIRREPTSSPLSYTTDGNVTVESDGLW 269
QY 61 NNNQTQLFLEHSLLTANTTKG 81
DB 270 NNNQTQLFLEHSLLTANTTKG 290

RESULT 4
AAO26679
ID AAO26679 standard; protein; 334 AA.
XX
AC AAO26679;
XX
DT 20-MAR-2003 (first entry)
XX
DE KIM-1 related protein, SEQ ID No 7.
XX
KW Cytostatic; gene therapy; antibody; antigen; antigen-binding;
KW proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;
KW renal disease; injury; renal cancer; human.
XX
OS Homo sapiens.
XX
PN WO200298920-A1.
XX
PD 12-DEC-2002.
XX
PF 31-MAY-2002; 2002WO-US017402.
XX
PR 01-JUN-2001; 2001US-0295449P.
PR 04-JUN-2001; 2001US-0295907P.
XX
PA (BIOJ) BIOGEN INC.
PA (GEO) GEN HOSPITAL CORP.
XX
PI Bailly V, Bonventre J;
XX
DR WPI; 2003-156845/15.
XX
PT New antibody, antibody derivative or antigen-binding polypeptide that
PT inhibits proteolytic release of a soluble kidney injury molecule-1
PT polypeptide, useful for treating or preventing renal disease or injury,
PT e.g. renal cancer.
XX
PS Disclosure; Page 39-40; 42pp; English.
XX
CC The invention relates to a novel antibody, antibody derivative or antigen

CC -binding polypeptide that inhibits proteolytic release of a soluble
CC kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.
CC The antibody, antibody derivative or antigen-binding polypeptide is
CC useful for treating or preventing renal disease or injury, e.g. renal
CC cancer. The antibody is also useful for inhibiting shedding of the KIM-1
CC polypeptide. This sequence represents a protein relating to the KIM-1
XX protein of the invention
SQ Sequence 334 AA;

Query Match 100.0%; Score 432; DB 6; Length 334;
Best Local Similarity 100.0%; Pred. No. 9.3e-36;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPLPRQHPEVATSPSSPOPAETHPTTLQGAIRREPTSSPLSYTTDGNVTVESDGLW 60
DB 210 MPLPRQHPEVATSPSSPOPAETHPTTLQGAIRREPTSSPLSYTTDGNVTVESDGLW 269
QY 61 NNNQTQLFLEHSLLTANTTKG 81
DB 270 NNNQTQLFLEHSLLTANTTKG 290

RESULT 5
ADO76696
ID ADO76696 standard; protein; 334 AA.
XX
AC ADO76696;
XX
DT 16-DEC-2004 (first entry)
XX
DE Human kidney injury molecule-1 (KIM-1).
XX
KW Human; KIM-1; kidney injury molecule-1; immunosuppressive; protozoacide;
KW muscular-gen.; neuroprotective; antinaemic; antithyroid; haemostatic;
KW antiallergic; antiinflammatory; vasotropic; nephrotropic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT Modified-site /label= Signal_peptide
FT Modified-site /note= "N-glycosylated" 65..67
FT Modified-site 258..260
FT Modified-site /note= "N-glycosylated" 272..274
FT Modified-site /note= "N-glycosylated" 286..288
FT Modified-site /note= "N-glycosylated" 290..311
FT Domain /note= "Transmembrane domain"
FT Region 324..334
FT /note= "C-terminal region unique to this splice variant"
XX
PN WO2004060041-A2.
XX
PD 22-JUL-2004.
XX
PF 29-DEC-2003; 2003WO-US041294.
XX
PR 30-DEC-2002; 2002US-0436934P.
XX
PA (BIOG-) BIOGEN IDEC MA INC.
XX
PI Rennert PD;
XX
DR WPI; 2004-534277/51.
XX
PT Use of a kidney injury molecule-1 (KIM-1) antagonist for e.g. treating
PT Th2 cell-mediated diseases or inflammatory diseases, inhibiting B cell
PT activation, or inhibiting production of a subset of antibodies against
PT one or more antigens.

XX PS Disclosure; SEQ ID NO 1; 68pp; English.

XX CC The present sequence is that of human kidney injury molecule-1 (KIM-1), a

CC type I cell membrane glycoprotein and member of the T cell immunoglobulin

CC (Ig) and mucin domain (TIM) family. This protein has 334 amino acids or

CC 359 amino acids ADQ76690, depending on splice variation. It has been

CC discovered that treatment of a mammal with a KIM-1 antagonist alters the

CC interaction of T cells and other immune system cells, e.g. dendritic

CC cells, monocytes, macrophages and B cells, and thereby strongly

CC suppresses an IgG response to an antigen. Such treatment also eliminates

CC IgG1 production by memory B cells in response to subsequent challenge

CC with the antigen. Blockage of the binding of KIM-1 to its receptor

CC reduces secretion of interferon-gamma by immune cells engaged in an

CC antigen response in the mixed lymphocyte response assay. Based on these

CC discoveries, the invention provides methods for therapeutically

CC modulating immune function in autoimmune diseases and other disorders of

CC the mammalian immune system. A method is claimed for inhibiting

CC signalling between a T cell and a second cell, e.g. an antigen-presenting

CC cell, in a mammal. The method involves identifying a mammal with an

CC immune disease or disorder, or one preparing to receive a tissue graft,

CC and administering a KIM-1 antagonist, especially a polypeptide

CC comprising: a KIM-1 Ig domain, and lacking a transmembrane domain and a

CC KIM-1 cytoplasmic domain; an anti-KIM-1 antibody; or an antigen-binding

CC fragment of an anti-KIM-1 antibody. Preferably, the KIM-1 antagonist is a

CC soluble polypeptide, which can include a KIM-1 mucin domain in addition

CC to the KIM Ig domain, and may include a heterologous moiety such as an Fc

CC moiety. The antagonist may be conjugated to a polymer such as

CC polyethylene glycol. The KIM-1 antagonist is used in methods of:

CC inhibiting activation of a B cell in a mammal; inhibiting disease relapse

CC in an autoimmune disease; inhibiting epitope spreading in an autoimmune

CC disease; treating a Th2 cell-mediated disease (e.g. myasthenia gravis,

CC autoimmune haemolytic anaemia, Chagas disease, Grave's disease,

CC idiopathic thrombocytopenia purpura, Wegener's granulomatosis,

CC polyarteritis nodosa, rapidly progressive crescentic glomerulonephritis,

CC graft-versus-host disease, or systemic lupus nephritis) or inflammatory

CC disease or disorder (e.g. inflammatory bowel diseases such as Crohn's

CC disease, ulcerative colitis, and ileitis); and inhibiting secretion of

CC IFN-gamma by lymphocytes.

XX SQ Sequence 334 AA;

Query Match 100.0%; Score 432; DB 8; Length 334;

Best Local Similarity 100.0%; Pred. No. 9.3e-36;

Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPLPRQNHVPATSPSPQPAETHPTTLQGAIRREPTSSPLYSYTTDNDVTSSDGLW 60

Db 210 MPLPRQNHVPATSPSPQPAETHPTTLQGAIRREPTSSPLYSYTTDNDVTSSDGLW 269

Qy 61 NNNQTQLFLEHSLLTANTTKG 81

Db 270 NNNQTQLFLEHSLLTANTTKG 290

RESULT 6

ADE36618

ID ADE36618 standard; protein; 339 AA.

XX AC ADE36618;

XX DT 29-JAN-2004 (first entry)

XX DE Plasmid pCR2.1-CG57008-03-S843 15B protein insert SEQ ID NO:28.

XX KW human; NOVX; cytostatic; antiinflammatory; gene therapy; vaccine;

XX KW renal cancer; inflammation; tissue typing.

XX OS Synthetic.

XX OS Homo sapiens.

XX FN WO2003080856-A2.

XX

PD 02-OCT-2003.

XX PF 19-MAR-2003; 2003WO-US008490.

XX PR 19-MAR-2002; 2002US-0365491P.

XX PR 13-SEP-2002; 2002US-0410618P.

XX PA (CURA-) CURAGEN CORP.

XX PI Lepley DM, Rieger DK, Tse K, Rastelli L, Smithson G, Mesri M;

PI Ooi CE, Anderson DW, Guo X, Giot L, Starling G;

XX DR WPI; 2003-876927/81.

XX DR N-PSDB; ADE36617.

XX PT New polypeptide, useful for preparing a composition for treating or

PT preventing a pathology associated with NOVX polypeptide e.g. renal cancer

PT or inflammation, or for tissue typing.

XX PS Example 1; SEQ ID NO 28; 239pp; English.

XX CC The present invention describes an isolated human NOVX polypeptide, where

CC X is Ia to Id or 2a to 2h, or its mature form, a sequence that is at

CC least 95 % identical to it, or a sequence comprising one or more

CC conservative substitutions in the amino acid sequence. The NOVX

CC polypeptide, and nucleic acid sequence encoding it, has cytostatic and

CC antiinflammatory activities, and can be used in gene therapy, and in

CC vaccines. The NOVX polypeptide is useful for preparing a composition for

CC treating or preventing a pathology associated with NOVX polypeptide e.g.

CC renal cancer or inflammation, or for tissue typing. The present sequence

CC represents a pCR2.1-CG57008-03-S843 15B protein insert, which is used in

CC an example from the present invention.

XX SQ Sequence 339 AA;

Query Match 100.0%; Score 432; DB 7; Length 339;

Best Local Similarity 100.0%; Pred. No. 9.5e-36;

Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPLPRQNHVPATSPSPQPAETHPTTLQGAIRREPTSSPLYSYTTDNDVTSSDGLW 60

Db 190 MPLPRQNHVPATSPSPQPAETHPTTLQGAIRREPTSSPLYSYTTDNDVTSSDGLW 249

Qy 61 NNNQTQLFLEHSLLTANTTKG 81

Db 250 NNNQTQLFLEHSLLTANTTKG 270

RESULT 7

ADE36592

ID ADE36592 standard; protein; 339 AA.

XX AC ADE36592;

XX DT 29-JAN-2004 (first entry)

XX DE Human NOV1a protein SEQ ID NO:2.

XX KW human; NOVX; cytostatic; antiinflammatory; gene therapy; vaccine;

XX KW renal cancer; inflammation; tissue typing.

XX OS Homo sapiens.

XX FN WO2003080856-A2.

XX PD 02-OCT-2003.

XX PF 19-MAR-2003; 2003WO-US008490.

XX PR 19-MAR-2002; 2002US-0365491P.

XX PR 13-SEP-2002; 2002US-0410618P.

XX PA (CURA-) CURAGEN CORP.

XX
PI Lepley DM, Rieger DK, Tse K, Rastelli L, Smithson G, Mesri M;
PI Ooi CS, Anderson DW, Guo X, Giot L, Starling G;
XX
XX WPI; 2003-876927/81.
DR N-PSDB; ADE36591.
DR
XX
XX New polypeptide, useful for preparing a composition for treating or
PT preventing a pathology associated with NOVX polypeptide e.g. renal cancer
PT or inflammation, or for tissue typing.
XX
XX
PS Claim 1; SEQ ID NO 2; 239pp; English.
XX
XX The present invention describes an isolated human NOVX polypeptide, where
CC X is 1a to 1d or 2a to 2h, or its mature form, a sequence that is at
CC least 95 % identical to it, or a sequence comprising one or more
CC conservative substitutions in the amino acid sequence. The NOVX
CC polypeptide, and nucleic acid sequence encoding it, has cytostatic and
CC antiinflammatory activities, and can be used in gene therapy, and in
CC vaccines. The NOVX polypeptide is useful for preparing a composition for
CC treating or preventing a pathology associated with NOVX polypeptide e.g.
CC renal cancer or inflammation, or for tissue typing. The present sequence
CC represents human NOV1a from the present invention.
XX
XX Sequence 339 AA;
SQ
Query Match 100.0%; Score 432; DB 7; Length 339;
Best Local Similarity 100.0%; Pred. No. 9.5e-36;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFLPRQNHPEVATSPSSPQPAETHPTTLOGAIRREPTSSPLYSTTGDNDVTTESSDGLW 60
Db 190 MFLPRQNHPEVATSPSSPQPAETHPTTLOGAIRREPTSSPLYSTTGDNDVTTESSDGLW 249
QY 61 NNNQTLFLEHSLTANTTKG 81
Db 250 NNNQTLFLEHSLTANTTKG 270
RESULT 8
ABR58582
ID ABR58582 standard; protein; 359 AA.
XX
AC ABR58582;
XX
XX 09-JUL-2003 (first entry)
XX
DE Human cancer related protein SEQ ID NO:239.
XX
XX Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
KW heart disease; atherosclerosis; endometriosis.
XX
OS Homo sapiens.
XX
FN WO2003025138-A2.
XX
XX 27-MAR-2003.
XX
XX 17-SEP-2002; 2002WO-US029560.
XX
PR 17-SEP-2001; 2001US-0323469P.
PR 20-SEP-2001; 2001US-0323887P.
PR 13-NOV-2001; 2001US-0350666P.
PR 08-FEB-2002; 2002US-0355145P.
PR 08-FEB-2002; 2002US-0355257P.
PR 12-APR-2002; 2002US-037246P.
XX
XX (BOS-) EOS BIOTECHNOLOGY INC.
XX
XX Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
PI Zlotnik A;
XX
XX WPI; 2003-354600/33.
DR

DR N-PSDB; ACC72709.
XX
XX New genes that are up-regulated or down-regulated in cancers, useful as
PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
PT therapeutic targets for screening drugs for treating these diseases.
XX
XX Claim 12; Page 742; 767pp; English.
XX
XX The present invention describes an isolated nucleic acid molecule, which
CC comprises the sequence of any of the genes that are up-regulated or down-
CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
CC acute lymphocytic leukemia). ACC72860 represent cancer
CC related gene nucleotide sequences which encode the proteins given in
CC ABR58521 to ABR58709. Also described: (1) determining the presence or
CC absence of a pathological cell in a patient; (2) an expression vector
CC comprising a nucleic acid molecule described above; (3) a host cell
CC comprising the vector; (4) an isolated polypeptide, which is encoded by
CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
CC of (4); (6) specifically targeting a compound to a pathological cell in a
CC patient by administering to the patient the antibody above; and (7) a
CC drug screening assay. The nucleic acid is useful as diagnostic markers or
CC therapeutic targets. In particular, the nucleic acid is useful for
CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
CC atherosclerosis and endometriosis. The nucleic acid is also useful in
CC drug screening, particularly for identifying agents for treating these
CC pathologies
XX
XX Sequence 359 AA;
SQ
Query Match 100.0%; Score 432; DB 6; Length 359;
Best Local Similarity 100.0%; Pred. No. 1e-35;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFLPRQNHPEVATSPSSPQPAETHPTTLOGAIRREPTSSPLYSTTGDNDVTTESSDGLW 60
Db 210 MFLPRQNHPEVATSPSSPQPAETHPTTLOGAIRREPTSSPLYSTTGDNDVTTESSDGLW 269
QY 61 NNNQTLFLEHSLTANTTKG 81
Db 270 NNNQTLFLEHSLTANTTKG 290
RESULT 9
ABP70439
ID ABP70439 standard; protein; 359 AA.
XX
AC ABP70439;
XX
XX 22-APR-2003 (first entry)
XX
DE Amino acid sequence of human TIM-1 allele 1.
XX
XX T cell immunoglobulin domain; mucin domain; TIM; TIM-1; TIM-2; TIM-3;
KW TIM-4; immune dysfunction; chromosome 5; malignancy; allergy; eczema;
KW myelodysplastic syndrome; airway hyperreactivity; cancer; asthma;
KW allergic T cell response; autoimmune disease.
XX
OS Homo sapiens.
XX
XX WO2003002722-A2.
XX
XX 09-JAN-2003.
XX
XX 01-JUL-2002; 2002WO-US020890.
XX
XX 29-JUN-2001; 2001US-0302344P.
XX
XX (STRD) UNIV LELAND STANFORD JUNIOR.
XX
XX McIntire JJ, Dekruyff RH, Umetsu DT, Freeman GJ, Kuchroo V;
XX

CC The present invention describes a method for detecting a bladder cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence that is 80 % identical to a table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059 encode the human bladder cancer-associated proteins given in ABR48146 to ABR48242). Bladder cancer-associated sequences from the present invention have cytostatic activities, and can be used in antisense gene therapy and in vaccine production. The method can be used for detecting a bladder cancer-associated transcript in a cell from a patient. The method is useful in diagnosing or treating bladder cancer and in screening for compounds that modulate bladder cancer, such as hormones or antibodies. The nucleic acid molecules from the present invention may be used in various screening and diagnostic methods, and for gene therapy, vaccine and/or antisense/inhibition applications

XX
SQ Sequence 359 AA;

Query Match 100.0%; Score 432; DB 6; Length 359;
Best Local Similarity 100.0%; Pred. No. 1e-35;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPLPRQNHPEVATSPSPQPAETHPTTLOGAIRREPTSSPLSYTTDGNVTVESSDGLW 60
|||||
DB 210 MPLPRQNHPEVATSPSPQPAETHPTTLOGAIRREPTSSPLSYTTDGNVTVESSDGLW 269

QY 61 NNNQTQLFLEHSLTANTTKG 81
|||||
DB 270 NNNQTQLFLEHSLTANTTKG 290

RESULT 12
AAO26680
ID AAO26680 standard; protein; 359 AA.

XX AAO26680;

XX 20-MAR-2003 (first entry)

XX KIM-1 related protein, SEQ ID No 8.

XX Cytostatic; gene therapy; antibody; antigen; antigen-binding;
KW proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;
KW renal disease; injury; renal cancer; human.

XX Homo sapiens.

XX WO200298920-A1.

XX 12-DEC-2002.

XX 31-MAY-2002; 2002WO-US017402.

PR 01-JUN-2001; 2001US-0295449P.

PR 04-JUN-2001; 2001US-0295907P.

XX (BIOJ) BIOGEN INC.

PA (GEO) GEN HOSPITAL CORP.

XX Bailly V, Bonventre J;

XX WPI; 2003-156845/15.

PT New antibody, antibody derivative or antigen-binding polypeptide that inhibits proteolytic release of a soluble kidney injury molecule-1 polypeptide, useful for treating or preventing renal disease or injury, e.g. renal cancer.

XX Disclosure; Page 40-41; 42pp; English.

XX The invention relates to a novel antibody, antibody derivative or antigen-binding polypeptide that inhibits proteolytic release of a soluble kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.

CC The antibody, antibody derivative or antigen-binding polypeptide is useful for treating or preventing renal disease or injury, e.g. renal cancer. The antibody is also useful for inhibiting shedding of the KIM-1 polypeptide. This sequence represents a protein relating to the KIM-1 protein of the invention

XX
SQ Sequence 359 AA;

Query Match 100.0%; Score 432; DB 6; Length 359;
Best Local Similarity 100.0%; Pred. No. 1e-35;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPLPRQNHPEVATSPSPQPAETHPTTLOGAIRREPTSSPLSYTTDGNVTVESSDGLW 60
|||||
DB 210 MPLPRQNHPEVATSPSPQPAETHPTTLOGAIRREPTSSPLSYTTDGNVTVESSDGLW 269

QY 61 NNNQTQLFLEHSLTANTTKG 81
|||||
DB 270 NNNQTQLFLEHSLTANTTKG 290

RESULT 13

ADE36594
ID ADE36594 standard; protein; 359 AA.

XX ADE36594;

XX 29-JAN-2004 (first entry)

XX Human NOV1b protein SEQ ID NO:4.

XX human; NOVX; cytostatic; antiinflammatory; gene therapy; vaccine;
KW renal cancer; inflammation; tissue typing.

XX Homo sapiens.

XX WO2003080856-A2.

XX 02-OCT-2003.

XX 19-MAR-2003; 2003WO-US008490.

XX 19-MAR-2002; 2002US-0365491P.

PR 13-SEP-2002; 2002US-0410618P.

XX (CURA-) CURAGEN CORP.

XX Lepley DM, Rieger DK, Tse K, Rastelli L, Smithson G, Mesri M;

PI Ooi CE, Anderson DW, Guo X, Giot L, Starling G;

XX WPI; 2003-876927/81.

XX N-PSDB; ADE36593.

XX New polypeptide, useful for preparing a composition for treating or preventing a pathology associated with NOVX polypeptide e.g. renal cancer or inflammation, or for tissue typing.

XX Claim 1; SEQ ID NO 4; 239pp; English.

XX The present invention describes an isolated human NOVX polypeptide, where X is 1a to 1d or 2a to 2h, or its mature form, a sequence that is at least 95 % identical to it, or a sequence comprising one or more conservative substitutions in the amino acid sequence. The NOVX polypeptide, and nucleic acid sequence encoding it, has cytostatic and antiinflammatory activities, and can be used in gene therapy, and in vaccines. The NOVX polypeptide is useful for preparing a composition for treating or preventing a pathology associated with NOVX polypeptide e.g. renal cancer or inflammation, or for tissue typing. The present sequence represents human NOV1b from the present invention.

XX Sequence 359 AA;

Query Match 100.0%; Score 432; DB 7; Length 359;

Best Local Similarity 100.0%; Pred. No. 1e-35;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPLPRQNHVPATSSPPQPAETHPTTLOGAIRRPTSPPLSYTTDGNNTVTSSDGLW 60
DB 210 MPLPRQNHVPATSSPPQPAETHPTTLOGAIRRPTSPPLSYTTDGNNTVTSSDGLW 269

QY 61 NNNQTLFLEHSLTANTTKG 81
DB 270 NNNQTLFLEHSLTANTTKG 290

RESULT 14
ADN38984
ID ADN38984 standard; protein; 359 AA.
XX ADN38984;
AC ADN38984;
XX
XX 17-JUN-2004 (first entry)
XX Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:302.
DE
DE
XX Human; differential expression; cancer; angiogenic disorder;
XX fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW retinal neovascularisation syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW vulneryary; gene therapy; vaccine.
XX
XX Homo sapiens.
OS
OS WO2003042661-A2.
PN
PN 22-MAY-2003.
PD
PD
PF 13-NOV-2002; 2002WO-US036810.
PF
XX 13-NOV-2001; 2001US-0350666P.
PR 21-NOV-2001; 2001US-0332464P.
PR 29-NOV-2001; 2001US-0334393P.
PR 03-DEC-2001; 2001US-0335394P.
PR 14-DEC-2001; 2001US-0340376P.
PR 08-JAN-2002; 2002US-0347211P.
PR 10-JAN-2002; 2002US-0347349P.
PR 08-FEB-2002; 2002US-035250P.
PR 13-FEB-2002; 2002US-0356714P.
PR 20-FEB-2002; 2002US-0359077P.
PR 29-MAR-2002; 2002US-0368809P.
PR 04-APR-2002; 2002US-0370110P.
PR 12-APR-2002; 2002US-0372246P.
PR 05-JUN-2002; 2002US-0386614P.
PR 16-JUL-2002; 2002US-0396839P.
PR 22-JUL-2002; 2002US-0397775P.
PR 22-JUL-2002; 2002US-0397845P.
PR 09-SEP-2002; 2002US-0409450P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
PA
XX Afar D, Aziz N, Ginsburg WM, Gish KC, Glynne R, Hevezi PA;
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX
XX WPI: 2003-468649/44.
DR N-PSDB; ADN38983.
DR
XX Determining the presence or absence of a pathological cell in a patient,
PT useful for diagnosing, prognosing or treating cancer, comprises detecting
PT a nucleic acid in a biological sample.
XX
XX Claim 12; SEQ ID NO 302; 1385pp; English.
PS
XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC

CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularisation syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a polypeptide of the invention.
XX
SQ Sequence 359 AA;

Query Match 100.0%; Score 432; DB 7; Length 359;
Best Local Similarity 100.0%; Pred. No. 1e-35;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPLPRQNHVPATSSPPQPAETHPTTLOGAIRRPTSPPLSYTTDGNNTVTSSDGLW 60
DB 210 MPLPRQNHVPATSSPPQPAETHPTTLOGAIRRPTSPPLSYTTDGNNTVTSSDGLW 269

QY 61 NNNQTLFLEHSLTANTTKG 81
DB 270 NNNQTLFLEHSLTANTTKG 290

RESULT 15
ADQ76690
ID ADQ76690 standard; protein; 359 AA.
XX ADQ76690;
AC ADQ76690;
XX
XX 16-DEC-2004 (first entry)
XX Human kidney injury molecule-1 (KIM-1).
DE
DE Human; KIM-1; kidney injury molecule-1; immunosuppressive; protozoacide;
KW muscular-gen.; neuroprotective; antianaemic; antithyroid; haemostatic;
KW antiallergic; antiinflammatory; vasotropic; nephrotropic.
XX
XX Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT /label= Signal_peptide
FT Modified-site 65..67
FT /note= "N-glycosylated"
FT Modified-site 258..260
FT /note= "N-glycosylated"
FT Modified-site 272..274
FT /note= "N-glycosylated"
FT Modified-site 286..288
FT /note= "N-glycosylated"
FT Domain 290..311
FT /note= "Transmembrane domain"
FT Region 324..359
FT /note= "C-terminal region unique to this splice variant"
XX
XX WO2004060041-A2.
PN
XX 22-JUL-2004.
PD
XX 29-DEC-2003; 2003WO-US041294.
PF
XX 30-DEC-2002; 2002US-0436934P.
PR
XX (BIOG-) BIOGEN IDEC MA INC.
PA
XX

Rennett PD;
WPI; 2004-534277/51.

Use of a kidney injury molecule-1 (KIM-1) antagonist for e.g. treating Th2 cell-mediated diseases or inflammatory diseases, inhibiting B cell activation, or inhibiting production of a subset of antibodies against one or more antigens.

Disclosure; SEQ ID NO 1; 68pp; English.

The present sequence is that of human kidney injury molecule-1 (KIM-1), a type I cell membrane glycoprotein and member of the T cell immunoglobulin (Ig) and mucin domain (TIM) family. This protein has 334 amino acids ADQ76696 or 359 amino acids, depending on splice variation. It has been discovered that treatment of a mammal with a KIM-1 antagonist alters the interaction of T cells and other immune system cells, e.g. dendritic cells, monocytes, macrophages and B cells, and thereby strongly suppresses an IgG response to an antigen. Such treatment also eliminates IgM production by memory B cells in response to subsequent challenge with the antigen. Blockage of the binding of KIM-1 to its receptor reduces secretion of interferon-gamma by immune cells engaged in an antigen response in the mixed lymphocyte response assay. Based on these discoveries, the invention provides methods for therapeutically modulating immune function in autoimmune diseases and other disorders of the mammalian immune system. A method is claimed for inhibiting signalling between a T cell and a second cell, e.g. an antigen-presenting cell, in a mammal. The method involves identifying a mammal with an immune disease or disorder, or one preparing to receive a tissue graft, and administering a KIM-1 antagonist, especially a polypeptide comprising: a KIM-1 Ig domain, and lacking a transmembrane domain and a KIM-1 cytoplasmic domain; an anti-KIM-1 antibody; or an antigen-binding fragment of an anti-KIM-1 antibody. Preferably, the KIM-1 antagonist is a soluble polypeptide, which can include a KIM-1 mucin domain in addition to the KIM Ig domain, and may include a heterologous moiety such as an Fc moiety. The antagonist may be conjugated to a polymer such as polyethylene glycol. The KIM-1 antagonist is used in methods of: inhibiting activation of a B cell in a mammal; inhibiting disease relapse in an autoimmune disease; inhibiting epitope spreading in an autoimmune disease; treating a Th2 cell-mediated disease (e.g. myasthenia gravis, autoimmune haemolytic anaemia, Chagas disease, Grave's disease, idiopathic thrombocytopenia purpura, Wegener's granulomatosis, polyarthritis nodosa, rapidly progressive crescentic glomerulonephritis, graft-versus-host disease, or systemic lupus nephritis) or inflammatory disease or disorder (e.g. inflammatory bowel diseases such as Crohn's disease, ulcerative colitis, and ileitis); and inhibiting secretion of IFN-gamma by lymphocytes.

Sequence 359 AA;

	Query Match	100.0%	Score 432;	DB 8;	Length 359;
	Best Local Similarity	100.0%;	Pred. No. 1e-35;		
	Matches 81;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MPLPRQNHEPVATSPSSPQPAAETHPTTLQGAIRREPTSPLYSYTGDNDVTESDGLW	60		
Db	210	MPLPRQNHEPVATSPSSPQPAAETHPTTLQGAIRREPTSPLYSYTGDNDVTESDGLW	269		
QY	61	NNNOTQLFLEHSLLTANTTKG	81		
Db	270	NNNOTQLFLEHSLLTANTTKG	290		

Search completed: June 29, 2005, 09:09:06
Job time : 59.6071 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 08:58:20 ; Search time 50.7642 Seconds
(without alignments)
613.589 Million cell updates/sec

Title: US-10-718-321-6

Perfect score: 432

Sequence: 1 MFLPRQNHPEVATSSPPQ.....NNQTLFLEHSLLTANTTKG 81

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	432	100.0	81	17 US-10-718-321-6	Sequence 6, Appli
2	432	100.0	334	17 US-10-655-506-7	Sequence 7, Appli
3	432	100.0	334	17 US-10-718-321-7	Sequence 7, Appli
4	432	100.0	339	17 US-10-391-939A-2	Sequence 2, Appli
5	432	100.0	339	17 US-10-391-939A-28	Sequence 28, Appli
6	432	100.0	359	14 US-10-188-012-17	Sequence 17, Appli
7	432	100.0	359	14 US-10-188-012-19	Sequence 19, Appli
8	432	100.0	359	15 US-10-295-027-302	Sequence 302, Appli
9	432	100.0	359	15 US-10-188-832-64	Sequence 64, Appli
10	432	100.0	359	17 US-10-391-939A-4	Sequence 4, Appli
11	432	100.0	359	17 US-10-663-497-17	Sequence 17, Appli

12	432	100.0	359	17 US-10-663-497-19	Sequence 19, Appli
13	432	100.0	359	17 US-10-718-321-8	Sequence 8, Appli
14	432	100.0	359	17 US-10-847-918-25	Sequence 25, Appli
15	432	100.0	364	14 US-10-188-012-25	Sequence 25, Appli
16	432	100.0	364	17 US-10-663-497-25	Sequence 25, Appli
17	432	100.0	365	14 US-10-188-012-21	Sequence 21, Appli
18	432	100.0	365	17 US-10-663-497-21	Sequence 21, Appli
19	427	98.8	364	14 US-10-188-012-27	Sequence 27, Appli
20	427	98.8	364	17 US-10-663-497-27	Sequence 27, Appli
21	423	97.9	359	14 US-10-188-012-23	Sequence 23, Appli
22	423	97.9	359	17 US-10-663-497-23	Sequence 23, Appli
23	396	91.7	263	17 US-10-391-939A-6	Sequence 6, Appli
24	386	91.7	263	17 US-10-391-939A-32	Sequence 32, Appli
25	396	91.7	263	17 US-10-391-939A-39	Sequence 39, Appli
26	396	91.7	263	17 US-10-805-177-50	Sequence 50, Appli
27	99	22.9	18	17 US-10-718-321-1	Sequence 1, Appli
28	89	20.6	307	17 US-10-655-506-3	Sequence 3, Appli
29	78.5	18.2	141	15 US-10-425-114-52586	Sequence 52586, A
30	78.5	18.2	144	16 US-10-425-115-245392	Sequence 245392, A
31	77.5	17.9	418	16 US-10-437-963-182939	Sequence 182939, A
32	77	17.8	440	17 US-10-732-923-6588	Sequence 6588, Ap
33	77	17.8	441	17 US-10-732-923-6588	Sequence 6588, Ap
34	77	17.8	483	16 US-10-437-963-157601	Sequence 157601, A
35	76.5	17.7	282	14 US-10-188-012-3	Sequence 3, Appli
36	76.5	17.7	282	17 US-10-663-497-3	Sequence 3, Appli
37	76	17.6	647	16 US-10-821-273-6	Sequence 27, Appli
38	76	17.6	893	15 US-10-334-143-27	Sequence 6, Appli
39	76	17.6	2115	16 US-10-437-963-195579	Sequence 195579, A
40	75.5	17.5	235	16 US-10-425-115-331823	Sequence 331823, A
41	75.5	17.5	1588	16 US-10-437-963-189741	Sequence 189741, A
42	75	17.4	8360	14 US-10-132-134-34	Sequence 34, Appli
43	73	16.9	127	15 US-10-424-599-250789	Sequence 250789, A
44	73	16.9	579	16 US-10-437-963-151894	Sequence 151894, A
45	72.5	16.8	302	15 US-10-225-066A-778	Sequence 778, App

ALIGNMENTS

RESULT 1

US-10-718-321-6
; Sequence 6, Application US/10718321
; Publication No. US20050112117A1
; GENERAL INFORMATION:
; APPLICANT: Biogen Idec Ma Inc.
; APPLICANT: Bailly, Veronique
; APPLICANT: Bonventre, Joseph
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: Molecules and Methods for Inhibiting
; TITLE OF INVENTION: Shedding of KIM-1
; FILE REFERENCE: A124 US
; CURRENT APPLICATION NUMBER: US/10/718,321
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/295449
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/295907
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US02/17402
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-718-321-6

Query Match 100.0%; Score 432; DB 17; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.4e-36;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFLPRQNHPEVATSSPPQASTHTTLOGATRRRPTSSPLSYTTGNDTVTESDGLW 60
|||||

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Db 1 MPLPRQNEHPVATSPSSQPAAETHPTTLQGAIRREPTSSPLSYTTGNDGNTVTSSDGLW 60
QY 61 NNNQTLFLEHSLLTANTTKG 81
Db 61 NNNQTLFLEHSLLTANTTKG 81

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US-10-655-506-7
; Sequence 7, Application US/10655506
; Publication No. US20050089868A1
; GENERAL INFORMATION:
; APPLICANT: Michele Sanicola-Nadel
; Joseph V. Bonventre
; Catherine A. Hession
; Takaharu Ichimura
; Henry Wei
; Richard L. Cate
; TITLE OF INVENTION: MODULATORS OF TISSUE REGENERATION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/655,506
; FILING DATE: 04-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/197,970
; FILING DATE: 23-Nov-1998
; APPLICATION NUMBER: US 60/018,228
; FILING DATE: 24-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Levine, Leslie M.
; REGISTRATION NUMBER: 35,245
; REFERENCE/DOCKET NUMBER: A010 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 679-2810
; TELEFAX: (617) 679-2838
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 334 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-655-506-7

Query Match 100.0%; Score 432; DB 17; Length 334;
Best Local Similarity 100.0%; Pred. No. 7.6e-36;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPLPRQNEHPVATSPSSQPAAETHPTTLQGAIRREPTSSPLSYTTGNDGNTVTSSDGLW 60
Db 210 MPLPRQNEHPVATSPSSQPAAETHPTTLQGAIRREPTSSPLSYTTGNDGNTVTSSDGLW 269

QY 61 NNNQTLFLEHSLLTANTTKG 81
Db 270 NNNQTLFLEHSLLTANTTKG 290

RESULT 3
US-10-718-321-7
; Sequence 7, Application US/10718321
; Publication No. US20050112117A1
; GENERAL INFORMATION:
; APPLICANT: Biogen Idec Ma Inc.
; APPLICANT: Bailly, Veronique
; APPLICANT: Bonventre, Joseph
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: Molecules and Methods for Inhibiting
; FILE REFERENCE: A124 US
; CURRENT APPLICATION NUMBER: US/10/718,321
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/295449
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/295907
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US02/17402
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-718-321-7

Query Match 100.0%; Score 432; DB 17; Length 334;
Best Local Similarity 100.0%; Pred. No. 7.6e-36;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPLPRQNEHPVATSPSSQPAAETHPTTLQGAIRREPTSSPLSYTTGNDGNTVTSSDGLW 60
Db 210 MPLPRQNEHPVATSPSSQPAAETHPTTLQGAIRREPTSSPLSYTTGNDGNTVTSSDGLW 269

QY 61 NNNQTLFLEHSLLTANTTKG 81
Db 270 NNNQTLFLEHSLLTANTTKG 290

RESULT 4
US-10-391-939A-2
; Sequence 2, Application US/10391939A
; Publication No. US20050014687A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W.;
; APPLICANT: Giot, Loic ;
; APPLICANT: Guo, Xiaojia Sasha;
; APPLICANT: Lepley, Denise M.;
; APPLICANT: Mesri, Mehdi ;
; APPLICANT: Ooi, Chean Eng;
; APPLICANT: Rastelli, Luca ;
; APPLICANT: Rieger, Daniel K.;
; APPLICANT: Smithson, Glennda ;
; APPLICANT: Starling, Gary ;
; APPLICANT: Tse, Kam-Fai
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-048
; CURRENT APPLICATION NUMBER: US/10/391,939A
; CURRENT FILING DATE: 2003-03-19
; PRIOR APPLICATION NUMBER: 60/365,491
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/410,618
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 2
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-391-939A-2

Query Match 100.0%; Score 432; DB 17; Length 339;
Best Local Similarity 100.0%; Pred. No. 7.8e-36;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 MPLPRQNHVPATSPSPQPAETHPTTLOGAIRREPTSSPLSYTTGNDTVTESDGLW 60
Db 190 MPLPRQNHVPATSPSPQPAETHPTTLOGAIRREPTSSPLSYTTGNDTVTESDGLW 249
Qy 61 NNNQTLFLEHSLTANTTKG 81
Db 250 NNNQTLFLEHSLTANTTKG 270

RESULT 5
US-10-391-939A-28
; Sequence 28, Application US/10391939A
; Publication No. US20050014687A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W.;
; APPLICANT: Giot, Loic;
; APPLICANT: Guo, Xiaojia Sasha;
; APPLICANT: Lepley, Denise M.;
; APPLICANT: Mesri, Mehdi;
; APPLICANT: Ooi, Chean Eng;
; APPLICANT: Rastelli, Luca;
; APPLICANT: Rieger, Daniel K.;
; APPLICANT: Smithson, Glenda;
; APPLICANT: Starling, Gary;
; APPLICANT: Tse, Kam-Fai
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-048
; CURRENT APPLICATION NUMBER: US/10/391,939A
; CURRENT FILING DATE: 2003-03-19
; PRIOR APPLICATION NUMBER: 60/365,491
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/410,618
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Curoseqlist version 0.1
; SEQ ID NO 28
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-391-939A-28

Query Match 100.0%; Score 432; DB 17; Length 339;
Best Local Similarity 100.0%; Pred. No. 7.8e-36;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPLPRQNHVPATSPSPQPAETHPTTLOGAIRREPTSSPLSYTTGNDTVTESDGLW 60
Db 190 MPLPRQNHVPATSPSPQPAETHPTTLOGAIRREPTSSPLSYTTGNDTVTESDGLW 249
Qy 61 NNNQTLFLEHSLTANTTKG 81
Db 250 NNNQTLFLEHSLTANTTKG 270

RESULT 6
US-10-188-012-17
; Sequence 17, Application US/10188012
; Publication No. US20030124114A1
; GENERAL INFORMATION:
; APPLICANT: McIntire, Jennifer Jones
; APPLICANT: Umetsu, Dale T.
; APPLICANT: Dekruyff, Rosemarie
; APPLICANT: Kuchroo, Vijay
; APPLICANT: Freeman, Gordon J.
; TITLE OF INVENTION: T Cell Regulatory Genes and Methods of
; FILE REFERENCE: STAN-235
; CURRENT APPLICATION NUMBER: US/10/188,012
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/302,344
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 359
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(359)
; OTHER INFORMATION: TIM-1, allele 2
US-10-188-012-17

Query Match 100.0%; Score 432; DB 14; Length 359;
Best Local Similarity 100.0%; Pred. No. 8.3e-36;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPLPRQNHVPATSPSPQPAETHPTTLOGAIRREPTSSPLSYTTGNDTVTESDGLW 60
Db 210 MPLPRQNHVPATSPSPQPAETHPTTLOGAIRREPTSSPLSYTTGNDTVTESDGLW 269
Qy 61 NNNQTLFLEHSLTANTTKG 81
Db 270 NNNQTLFLEHSLTANTTKG 290

RESULT 7
US-10-188-012-19
; Sequence 19, Application US/10188012
; Publication No. US20030124114A1
; GENERAL INFORMATION:
; APPLICANT: McIntire, Jennifer Jones
; APPLICANT: Umetsu, Dale T.
; APPLICANT: Dekruyff, Rosemarie
; APPLICANT: Kuchroo, Vijay
; APPLICANT: Freeman, Gordon J.
; TITLE OF INVENTION: T Cell Regulatory Genes and Methods of
; FILE REFERENCE: STAN-235
; CURRENT APPLICATION NUMBER: US/10/188,012
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/302,344
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 359
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(359)
; OTHER INFORMATION: TIM-1, allele 2
US-10-188-012-19

Query Match 100.0%; Score 432; DB 14; Length 359;
Best Local Similarity 100.0%; Pred. No. 8.3e-36;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPLPRQNHVPATSPSPQPAETHPTTLOGAIRREPTSSPLSYTTGNDTVTESDGLW 60
Db 210 MPLPRQNHVPATSPSPQPAETHPTTLOGAIRREPTSSPLSYTTGNDTVTESDGLW 269
Qy 61 NNNQTLFLEHSLTANTTKG 81
Db 270 NNNQTLFLEHSLTANTTKG 290

RESULT 8
US-10-295-027-302
; Sequence 302, Application US/10295027
; Publication No. US2003023350A1
; GENERAL INFORMATION:
; APPLICANT: Afari, Daniel
; APPLICANT: Aziz, Natasha
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 359
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(360)
; OTHER INFORMATION: TIM-1 allele 1
US-10-188-012-17

Query Match 100.0%; Score 432; DB 14; Length 359;
Best Local Similarity 100.0%; Pred. No. 8.3e-36;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPLPRQNHVPATSPSPQPAETHPTTLOGAIRREPTSSPLSYTTGNDTVTESDGLW 60
Db 210 MPLPRQNHVPATSPSPQPAETHPTTLOGAIRREPTSSPLSYTTGNDTVTESDGLW 269
Qy 61 NNNQTLFLEHSLTANTTKG 81
Db 270 NNNQTLFLEHSLTANTTKG 290

RESULT 7
US-10-188-012-19
; Sequence 19, Application US/10188012
; Publication No. US20030124114A1
; GENERAL INFORMATION:
; APPLICANT: McIntire, Jennifer Jones
; APPLICANT: Umetsu, Dale T.
; APPLICANT: Dekruyff, Rosemarie
; APPLICANT: Kuchroo, Vijay
; APPLICANT: Freeman, Gordon J.
; TITLE OF INVENTION: T Cell Regulatory Genes and Methods of
; FILE REFERENCE: STAN-235
; CURRENT APPLICATION NUMBER: US/10/188,012
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/302,344
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 359
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(359)
; OTHER INFORMATION: TIM-1, allele 2
US-10-188-012-19

Query Match 100.0%; Score 432; DB 14; Length 359;
Best Local Similarity 100.0%; Pred. No. 8.3e-36;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPLPRQNHVPATSPSPQPAETHPTTLOGAIRREPTSSPLSYTTGNDTVTESDGLW 60
Db 210 MPLPRQNHVPATSPSPQPAETHPTTLOGAIRREPTSSPLSYTTGNDTVTESDGLW 269
Qy 61 NNNQTLFLEHSLTANTTKG 81
Db 270 NNNQTLFLEHSLTANTTKG 290

RESULT 8
US-10-295-027-302
; Sequence 302, Application US/10295027
; Publication No. US2003023350A1
; GENERAL INFORMATION:
; APPLICANT: Afari, Daniel
; APPLICANT: Aziz, Natasha
```

```
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 302
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-302

Query Match      100.0%; Score 432; DB 15; Length 359;
Best Local Similarity 100.0%; Pred. No. 8.3e-36;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPLPRQNHPEVATSSSPQPAETHPTTLQGAIRREPTSSPLSYTTDGNNDVTSSDGLW 60
   |||||||
Db 210 MPLPRQNHPEVATSSSPQPAETHPTTLQGAIRREPTSSPLSYTTDGNNDVTSSDGLW 269

QY 61 NNNQTLFLEHSLLTANTTKG 81
   |||||||
Db 270 NNNQTLFLEHSLLTANTTKG 290

RESULT 9
US-10-188-832-64
; Sequence 64, Application US/10188832
; Publication No. US20040076955A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Nataasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002330US
; CURRENT APPLICATION NUMBER: US/10/188,832
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
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; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-832-64

Query Match      100.0%; Score 432; DB 15; Length 359;
Best Local Similarity 100.0%; Pred. No. 8.3e-36;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPLPRQNHPEVATSSSPQPAETHPTTLQGAIRREPTSSPLSYTTDGNNDVTSSDGLW 60
   |||||||
Db 210 MPLPRQNHPEVATSSSPQPAETHPTTLQGAIRREPTSSPLSYTTDGNNDVTSSDGLW 269

QY 61 NNNQTLFLEHSLLTANTTKG 81
   |||||||
Db 270 NNNQTLFLEHSLLTANTTKG 290

RESULT 10
US-10-391-939A-4
; Sequence 4, Application US/10391939A
; Publication No. US20050014687A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W.;
; APPLICANT: Giot, Ioic ;
; APPLICANT: Guo, Xiaojia Sasha;
; APPLICANT: Lepley, Denise M.;
; APPLICANT: Mesri, Mehdi ;
; APPLICANT: Ooi, Chean Eng;
; APPLICANT: Rastelli, Luca ;
; APPLICANT: Rieger, Daniel K.;
; APPLICANT: Smithson, Glennda ;
; APPLICANT: Starling, Gary ;
; APPLICANT: Tse, Kam-Fai
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-048
; CURRENT APPLICATION NUMBER: US/10/391,939A
; CURRENT FILING DATE: 2003-03-19
; PRIOR APPLICATION NUMBER: 60/365,491
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/410,618
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 4
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-391-939A-4

Query Match      100.0%; Score 432; DB 17; Length 359;
Best Local Similarity 100.0%; Pred. No. 8.3e-36;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPLPRQNHPEVATSSSPQPAETHPTTLQGAIRREPTSSPLSYTTDGNNDVTSSDGLW 60
   |||||||
Db 210 MPLPRQNHPEVATSSSPQPAETHPTTLQGAIRREPTSSPLSYTTDGNNDVTSSDGLW 269

QY 61 NNNQTLFLEHSLLTANTTKG 81
   |||||||
Db 270 NNNQTLFLEHSLLTANTTKG 290

RESULT 11
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US-10-663-497-17
; Sequence 17, Application US/10663497
; Publication No. US20050095593A1
; GENERAL INFORMATION:
; APPLICANT: Dale Umetsu
; APPLICANT: Rosemarie DeKruyff
; APPLICANT: Jennifer McIntire
; APPLICANT: Gordon Freeman
; TITLE OF INVENTION: T CELL REGULATORY GENES ASSOCIATED WITH
; FILE REFERENCE: STAN-235CIP
; CURRENT APPLICATION NUMBER: US/10/663,497
; PRIOR FILING DATE: 2003-09-15
; PRIOR FILING DATE: 2001-06-29
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 359
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(360)
; OTHER INFORMATION: TIM-1 allele 1
US-10-663-497-17

Query Match      100.0%; Score 432; DB 17; Length 359;
Best Local Similarity 100.0%; Pred. No. 8.3e-36;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPLPRQNHPEVATSPSSQPAETHPTTLOGAIRREPTSSPLSYTTDGNDDVTTESSDGLW 60
Db 210 MPLPRQNHPEVATSPSSQPAETHPTTLOGAIRREPTSSPLSYTTDGNDDVTTESSDGLW 269

QY 61 NNNQTLFLEHSLLTANTTKG 81
Db 270 NNNQTLFLEHSLLTANTTKG 290

RESULT 12
US-10-663-497-19
; Sequence 19, Application US/10663497
; Publication No. US20050095593A1
; GENERAL INFORMATION:
; APPLICANT: Dale Umetsu
; APPLICANT: Rosemarie DeKruyff
; APPLICANT: Jennifer McIntire
; APPLICANT: Gordon Freeman
; TITLE OF INVENTION: T CELL REGULATORY GENES ASSOCIATED WITH
; FILE REFERENCE: STAN-235CIP
; CURRENT APPLICATION NUMBER: US/10/663,497
; PRIOR FILING DATE: 2003-09-15
; PRIOR FILING DATE: 2001-06-29
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 359
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(359)
; OTHER INFORMATION: TIM-1, allele 2
US-10-663-497-19

Query Match      100.0%; Score 432; DB 17; Length 359;
Best Local Similarity 100.0%; Pred. No. 8.3e-36;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPLPRQNHPEVATSPSSQPAETHPTTLOGAIRREPTSSPLSYTTDGNDDVTTESSDGLW 60
Db 210 MPLPRQNHPEVATSPSSQPAETHPTTLOGAIRREPTSSPLSYTTDGNDDVTTESSDGLW 269

QY 61 NNNQTLFLEHSLLTANTTKG 81
Db 270 NNNQTLFLEHSLLTANTTKG 290

RESULT 13
US-10-718-321-8
; Sequence 8, Application US/10718321
; Publication No. US20050112117A1
; GENERAL INFORMATION:
; APPLICANT: Biogen Idec Ma Inc.
; APPLICANT: Bonventre, Joseph
; APPLICANT: Bailly, Veronique
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: Molecules and Methods for Inhibiting
; FILE REFERENCE: A124 US
; CURRENT APPLICATION NUMBER: US/10/718,321
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/295449
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/295907
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US02/17402
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-718-321-8

Query Match      100.0%; Score 432; DB 17; Length 359;
Best Local Similarity 100.0%; Pred. No. 8.3e-36;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPLPRQNHPEVATSPSSQPAETHPTTLOGAIRREPTSSPLSYTTDGNDDVTTESSDGLW 60
Db 210 MPLPRQNHPEVATSPSSQPAETHPTTLOGAIRREPTSSPLSYTTDGNDDVTTESSDGLW 269

QY 61 NNNQTLFLEHSLLTANTTKG 81
Db 270 NNNQTLFLEHSLLTANTTKG 290

RESULT 14
US-10-847-918-25
; Sequence 25, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 359
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-847-918-25

Query Match      100.0%; Score 432; DB 17; Length 359;
Best Local Similarity 100.0%; Pred. No. 8.3e-36;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPLPRNHPEVATSPSSPOPAETHPTTLOGAIRREPTSSPLSYTTDGNDDVTTESSDGLW 60
DB 210 MPLPRNHPEVATSPSSPOPAETHPTTLOGAIRREPTSSPLSYTTDGNDDVTTESSDGLW 269

QY 61 NNNQTQFLFHSLLTANTTKG 81
DB 270 NNNQTQFLFHSLLTANTTKG 290
```

```

RESULT 15
US-10-188-012-25
; Sequence 25, Application US/10188012
; Publication No. US20030124114A1
; GENERAL INFORMATION:
; APPLICANT: McIntire, Jennifer Jones
; APPLICANT: Umetsu, Dale T.
; APPLICANT: Dekruyff, Rosemarie
; APPLICANT: Kuchroo, Vijay
; APPLICANT: Freeman, Gordon J.
; TITLE OF INVENTION: T Cell Regulatory Genes and Methods of
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: STAN-235
; CURRENT APPLICATION NUMBER: US/10/188,012
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/302,344
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 364
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(364)
; OTHER INFORMATION: TIM-1 allele 5
US-10-188-012-25
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Query Match      100.0%; Score 432; DB 14; Length 364;
Best Local Similarity 100.0%; Pred. No. 8.5e-36;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPLPRNHPEVATSPSSPOPAETHPTTLOGAIRREPTSSPLSYTTDGNDDVTTESSDGLW 60
DB 215 MPLPRNHPEVATSPSSPOPAETHPTTLOGAIRREPTSSPLSYTTDGNDDVTTESSDGLW 274

QY 61 NNNQTQFLFHSLLTANTTKG 81
DB 275 NNNQTQFLFHSLLTANTTKG 295
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Search completed: June 29, 2005, 09:33:00
Job time : 51.7642 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 08:57:16 ; Search time 7.32024 Seconds
(without alignments)
1064.659 Million cell updates/sec

Title: US-10-718-321-6
Perfect score: 432
Sequence: 1 MFLPRQNHVPVATSPSPQP.....NNQTQLFLEHSLLTANTTKG 81
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	348	80.6	451	2 S71754	cellular hepatitis
2	79.5	18.4	1007	2 T24643	hypothetical prote
3	76	17.6	1006	2 T42731	atrophin-1 relat
4	72.5	16.8	1082	2 T43204	chromatin structur
5	72	16.7	235	2 FC2022	mucin like protein
6	72	16.7	1402	2 I46707	translation initia
7	72	16.7	1777	2 T34369	hypothetical prote
8	71	16.4	1131	2 T15787	hypothetical prote
9	70.5	16.3	644	2 S39356	transcription fact
10	70.5	16.3	648	2 T20144	hypothetical prote
11	70.5	16.3	1095	2 FC1114	SKCDC25 protein -
12	70	16.2	321	2 T45053	SAC7 protein - yea
13	70	16.2	654	2 S63673	probable outer mem
14	69.5	16.1	479	2 G71957	chitinase (EC 3.2.
15	69.5	16.1	542	2 I39540	probable low-affin
16	69.5	16.1	574	2 T05964	acetylcholine rece
17	69	16.0	602	2 A45769	fibrogen-binding
18	69	16.0	1166	2 T28680	nuclear pore compl
19	69	16.0	1317	2 A54831	hypothetical prote
20	68.5	15.9	213	2 T01715	probable myb-relat
21	68.5	15.9	285	2 G85016	type 1 transmembra
22	68.5	15.9	681	2 A45705	evolved beta-D-gal
23	68.5	15.9	1042	2 E85968	evolved beta-D-gal
24	68.5	15.9	1042	2 F91123	hypothetical prote
25	68.5	15.9	1370	2 T19188	hypothetical prote
26	68.5	15.9	2241	2 T20971	hypothetical prote
27	68.5	15.9	2261	2 T20978	hypothetical prote
28	68	15.7	310	2 T45873	hypothetical prote
29	68	15.7	405	2 H89930	protein RliG11.14

30	68	15.7	620	2 A70525	hypothetical prote
31	68	15.7	1056	2 A53767	mucin MUC5B, trach
32	68	15.7	2018	2 T34274	hypothetical prote
33	67.5	15.6	137	2 G96017	conserved hypotet
34	67.5	15.6	1419	2 T30531	agglutinin-like ad
35	67	15.5	447	2 T18447	hrpW protein - Erw
36	67	15.5	1015	2 JC6552	DNA topoisomerase
37	67	15.5	1186	2 T19050	hypothetical prote
38	67	15.5	1560	2 T42727	proliferation pote
39	66.5	15.4	322	2 T23891	hypothetical prote
40	66.5	15.4	398	2 S50507	excision repair pr
41	66.5	15.4	575	2 S39484	DNA-binding protei
42	66.5	15.4	881	2 T28013	hypothetical prote
43	66.5	15.4	1589	2 C44766	defective chorion-
44	66	15.3	437	2 S15704	transforming prote
45	66	15.3	575	2 JC7794	lammer kinase homo

ALIGNMENTS

RESULT 1
S71754
cellular hepatitis A receptor HAVcr-1 precursor - green monkey
N;Alternate names: surface glycoprotein
C:Species: Cercopithecus aethiops (green monkey, grivet)
C>Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004
C:Accession: S71754
R:Kaplan, G.; Totenuka, A.; Thompson, P.; Akatsuka, T.; Moritsugu, Y.; Feinstein, S.M.
EMBO J. 15, 4282-4296, 1996
A:Title: Identification of a surface glycoprotein on African green monkey kidney cells as
A:Reference number: S71754; MUID:97015129; PMID:8861957
A:Accession: S71754
A:Molecule type: mRNA
A:Residues: 1-451 <KAP>
A:Cross-references: UNIPROT:Q95144; EMBL:X98252; NID:gl526573; PID:e247449; PID:gl526574
A:Experimental source: kidney
C:Keywords: glycoprotein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-451/Product: cellular hepatitis A receptor HAVcr-1 #status predicted <MAT>

Query Match 80.6%; Score 348; DB 2; Length 451;
Best Local Similarity 82.5%; Pred. No. 1.5e-26;
Matches 66; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
Qy 2 PLPRQNHVPVATSPSPQPAETHPTTLOGAIRREPTSSPLSYVTDPGNDVTVESSDGLWN 61
Db 291 PLPMQNHVPVATSPSPQPAETHPTTLLGATRTQPTSSPLSYVTDPGNDVTVESSDGLWN 350
Qy 62 NNQTQLFLEHSLLTANTTKG 81
Db 351 NNQTQLSPHSPQWNTTEG 370

RESULT 2
T24643
hypothetical protein T07C12.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24643
R:McMurray, A.
A:Reference number: Z19916
submitted to the EMBL Data Library, June 1996
A:Accession: T24643
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1007 <WIL>
A:Cross-references: UNIPROT:Q22286; EMBL:Z73976; PIDN:CAA98287.1; GSPDB:GN00023; CESP:T07C12.8
A:Experimental source: clone T07C12
C:Genetics:
A:Gene: CESP:T07C12.8
A:Map position: 5
A:Introns: 137/1; 178/2; 275/1; 295/3; 336/2; 390/1; 747/1; 846/3; 890/1; 953/2


```

Qy 40 -----PLYSYTTD--GNDTVTSSDGLNNTQQLF 68
Db 221 DLGAAAVASAAYGWNTAYSGLPARSQFFYAQYASDYIGN-AVGMSSSAWFHQERLY 278

RESULT 10
T20144
hypothetical protein C52A11.1 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T20144
R:Sulston, J.
submitted to the EMBL Data Library, November 1994
A/Reference number: Z19229
A/Accession: T20144
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-648 <WIL>
A/Cross-references: EMBL:Z46792; PIDN:CAA86766.1; GSPDB:GN00020; CESP:C52A11.1
A/Experimental source: clone C52A11
C/Genetics:
A/Name: CESP:C52A11.1
A/Map position: 2
A/Introns: 87/3; 237/3; 272/2; 456/1; 565/1; 622/1

Query Match 16.3%; Score 70.5; DB 2; Length 648;
Best Local Similarity 32.6%; Pred. No. 36;
Matches 28; Conservative 10; Mismatches 19; Indels 29; Gaps 6;

Qy 8 HEP-----VATSPSSPOP-----AETH---PTTQGAIRREPTSSPLYS 43
Db 156 HEPKEPLKEVDTPILPOPVRTSKFEVTPVKEALHDAEPTSMPPK-APEPTAPLRR 214

Qy 44 YTTDNDT-VTESSDGLWN---NNQT 65
Db 215 LSTDSDTSFSGHSKDLFSPTNPQT 240

RESULT 11
PC1114
SKDC25 protein - yeast (Saccharomyces kluyveri) (fragment)
C/Species: Saccharomyces kluyveri
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: PC1114
R:Prigozy, T.; Gonzales, E.; Broek, D.
Gene 117, 67-72, 1992
A/Title: Identification and analysis of a DNA fragment from Saccharomyces kluyveri that
A/Reference number: PC1114; MUID:92354938; PMID:1644315
A/Accession: PC1114
A/Molecule type: DNA
A/Residues: 1-1095 <PRI>
A/Cross-references: UNIPROT:Q02342; GB:M82964; NID:G171186; PIDN:AAA34479.1; PID:G171187
C/Genetics:
A/Name: SKDC25
C/Keywords: transmembrane protein
F:808-1049/Domain: CDC25-type guanine nucleotide exchange activator homology <SOS>

Query Match 16.3%; Score 70.5; DB 2; Length 1095;
Best Local Similarity 23.1%; Pred. No. 69;
Matches 15; Conservative 19; Mismatches 28; Indels 3; Gaps 2;

Qy 4 PRONHEPV-ATSPSSPOPAETHPTTQGAIRREPTSSPLYSYTTDGNNDTVTESSDGLWNN 62
Db 104 PRDSKVITSTINTIPDFSRASATIPSLQNESPARPINFSSSTDTLTFSED--WQS 161

Qy 63 NQTOL 67
Db 162 NSPNL 166

RESULT 12
T45053

```

C:Species: Caenorhabditis elegans
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T45053
R:Wilson, R.; Ainscough, R.; Anderson, K.; Baynes, C.; Berks, M.; Bonfield, J.; Burton, R.; raser, A.; Fulton, L.; Gardner, A.; Green, P.; Hawkins, T.; Hillier, L.; Jier, M.; Johns, B.; O'Callaghan, M.; Parsons, J.; Percy, C.; Rifken, L.; Roopra, A.; Saunders, D. Nature 368, 32-38, 1994
A:Authors: Showkneen, R.; Sims, M.; Smaildon, N.; Smith, A.; Smith, M.; Sonnhammer, E.; Stock, L.; Wilkinson-Sproat, J.; Wohldman, P.
A>Title: 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.
A:Reference number: S43531; MUID:94150718; PMID:7906398
A:Accession: T45053
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-321 <WIL>
A:Cross-references: UNIPROT:Q9NET3; EMBL:AL132896; NID:g6434440; PIDN:CAB60932.1; PID:g6434440
A:Experimental source: clone Y39B6B
C:Genetics:
A:Map position: 3
A:Introns: 41/2; 95/2; 131/1; 170/3; 208/1; 236/2; 279/3
A:Note: Y39B6B.aa

Query Match 16.2%; Score 70; DB 2; Length 321;
Best Local Similarity 29.1%; Pred. No. 17;
Matches 23; Conservative 13; Mismatches 25; Indels 18; Gaps 4;

QY 3 LPRQNHPEVATSPSPQPAETHPTTLOGAIRREPTSSPLYSTTGDNDVTVESSD----G 58
DB 1 MPHQKYVDTRRYGVFVS---PSYHNG---RSMVSSDMYTTTDTNVTDSYANRAGCG 54

QY 59 LWNNTQTQLFLEHSLLTAN 77
DB 55 VW-----AKYGIFTAN 65

RESULT 13
S69673
SAC7 protein - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YDR389w
C:Species: Saccharomyces cerevisiae
C:Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C:Accession: S69673; A34712
R:Dieterich, F.S.
A:Submitted to the EMBL Data Library, July 1995
A:Description: The sequence of S. cerevisiae cosmids 9481, 9509, 9926, 9461, and lambda
A:Reference number: S69665
A:Accession: S69673
A:Molecule type: DNA
A:Residues: 1-654 <DIE>
A:Cross-references: UNIPROT:P17121; EMBL:U32274; NID:g927313; PID:g927322; MIPS:YDR389w
R:Dunn, T.M.; Shortle, D.
Mol. Cell. Biol. 10, 2308-2314, 1990
A>Title: Null alleles of SAC7 suppress temperature-sensitive actin mutations in Sacchar
A:Reference number: A34712; MUID:90220616; PMID:2183030
A:Accession: A34712
A:Molecule type: DNA
A:Residues: 247-497, 'LEMLLLVT', 506, 'EERVYSGYINREF' <DUN>
A:Cross-references: GB:M32335; NID:g172531; PIDN:AAA35016.1; PID:g172532
C:Genetics:
A:Gene: SGD:SAC7
A:Cross-references: SGD:S0002797; MIPS:YDR389w
A:Map position: 4R
C:Keywords: cytoskeleton

Query Match 16.2%; Score 70; DB 2; Length 654;
Best Local Similarity 35.5%; Pred. No. 41;
Matches 22; Conservative 3; Mismatches 31; Indels 6; Gaps 2;

QY 4 PRQNHPEVATSPSPQ--PAETHPTTLOGAIRREPTSSPLYSTTGDNDVTVESSDGLWN 61
DB 33 PKSMSESNITVPRSPSTLSRNQPTTL-----KRPLUSSRPYSINTPTDKRSFSKSAQN 88
QY 62 NN 63

C:Species: Helicobacter pylori (strain J99)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: G71957
A:Variety: strain J99
A:Species: Helicobacter pylori
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A>Title: Genomic sequence comparison of two unrelated isolates of the human gastric patho
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: G71957
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-479 <ARN>
A:Cross-references: UNIPROT:Q9ZMI3; GB:AE001461; GB:AE001439; NID:g4154749; PIDN:AAD05813
A:Experimental source: strain J99
C:Genetics:
A:Gene: jhp0237
C:Superfamily: Helicobacter pylori outer membrane protein omp20

Query Match 16.1%; Score 69.5; DB 2; Length 479;
Best Local Similarity 35.7%; Pred. No. 31;
Matches 25; Conservative 7; Mismatches 27; Indels 11; Gaps 3;

QY 14 SPSSPQPAETHPTTLOGAIRREPTSSPLYSTTD--GNDVTVESSDGLWNN-----N 63
DB 45 NPGFTQAOELQLIRDGAVRLQTSAPL-SYVLDILGNKTKTLLSESLKNNPQQNGQPN 103

QY 64 QTQLFLEHSL 73
DB 104 QALVNLEQSL 113

RESULT 15
I39540
chitinase (BC 3.2.1.14) II precursor - Aeromonas sp.
C:Species: Aeromonas sp.
C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
A:Accession: I39540
R:Ueda, M.; Kawaguchi, T.; Arai, M.
J. Ferment. Bioeng. 78, 205-211, 1994
A>Title: Molecular cloning and nucleotide sequence of the gene encoding chitinase II from
A:Reference number: I39540
A:Accession: I39540
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-542 <RES>
A:Cross-references: UNIPROT:Q59145; GB:D31818; NID:g499711; PIDN:BA06605.1; PID:g499712
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 16.1%; Score 69.5; DB 2; Length 542;
Best Local Similarity 27.5%; Pred. No. 36;
Matches 22; Conservative 10; Mismatches 45; Indels 3; Gaps 1;

QY 2 PLPRQNHPEVATSPSPQPAETHPTTLOGAIRREPTSSPLYSTTGDNDVTVESSDGLWN 61
DB 346 PAPTATPVGTGPTVTVPKPTTTPVPTTAPTATPKTATVPVPSSTT--CAATWSSSTAYN 402
QY 62 NNQTQLFLEHSLLTANTTKG 81
DB 403 GGATVAYNGHNYQAKWTTQG 422

Search completed: June 29, 2005, 08:58:11
Job time : 8.32024 secs

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OM protein - protein search, using sw model

Run on: June 29, 2005, 08:57:16 ; Search time 29.8703 Seconds
(without alignments)
543.815 Million cell updates/sec

Title: US-10-718-321-6_COPY_40_81

Perfect score: 225

Sequence: 1 PLYSYTGDNDVTSSDGL.....NNQTQLFLESLTANTYKG 42

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003Bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	225	100.0	81	6	AAO26678 Human KIM
2	225	100.0	298	8	Adq76693 Human KIM
3	225	100.0	334	2	AAW38336 Human kid
4	225	100.0	334	6	AAO26679 KIM-1 rel
5	225	100.0	334	8	Adq76696 Human kid
6	225	100.0	339	7	Ades36618 Plasmid p
7	225	100.0	339	7	Ades36592 Human NOV
8	225	100.0	359	6	ABR58582 Human can
9	225	100.0	359	6	ABP70439 Amino aci
10	225	100.0	359	6	ABP70438 Amino aci
11	225	100.0	359	6	ABR48174 Human bla
12	225	100.0	359	6	AAO26680 KIM-1 rel
13	225	100.0	359	7	Ades36594 Human NOV
14	225	100.0	359	7	ADN38984 Cancer/an
15	225	100.0	359	8	Adq76690 Human kid
16	225	100.0	364	6	ABP70442 Amino aci
17	225	100.0	365	6	ABP70440 Amino aci
18	225	100.0	518	8	Adq76691 Human KIM
19	220	97.8	359	6	ABP70441 Amino aci
20	220	97.8	364	6	ABP70443 Amino aci
21	189	84.0	263	7	Ades36629 Human NOV
22	189	84.0	263	7	Ades36622 Plasmid p
23	189	84.0	263	7	Ades36596 Human NOV
24	178	79.1	451	2	AAK92803 Hepatitis
25	101	44.9	18	6	AAO26686 Human KIM

26	99	44.0	18	6	AAO26687	AAO26687 Human KIM
27	99	44.0	18	6	AAO26673	AAO26673 Monoclonal
28	90	40.0	18	6	AAO26688	AAO26688 Human KIM
29	82	36.4	18	6	AAO26685	AAO26685 Human KIM
30	60	26.7	602	2	AAW51705	AAW51705 Neurotrop
31	60	26.7	602	2	AAW32900	AAW32900 Chicken n
32	60	26.7	606	4	AAW78898	AAW78898 C. glutam
33	60	26.7	1070	4	AAW48099	AAW48099 Amino aci
34	60	26.7	1070	4	AAW08550	AAW08550 Chicken n
35	58.5	26.0	774	8	ADG93320	ADG93320 DEN1 (Pue
36	58.5	26.0	775	8	ADG93318	ADG93318 DEN1 (Pue
37	58	25.8	981	5	AAW18306	AAW18306 Venezuela
38	57	25.3	207	2	AAW38334	AAW38334 Rat kidne
39	57	25.3	679	8	ADS41629	ADS41629 Bacterial
40	57	25.3	2399	6	ABU31130	ABU31130 Protein e
41	56.5	25.1	1658	5	ABB55478	ABB55478 Lactococc
42	56	24.9	219	3	AAW19395	AAW19395 Arabidops
43	56	24.9	249	3	AAW53467	AAW53467 Arabidops
44	56	24.9	249	3	AAW19394	AAW19394 Arabidops
45	56	24.9	268	3	AAW53466	AAW53466 Arabidops

ALIGNMENTS

RESULT 1
AAO26678
ID AAO26678 standard; protein; 81 AA.
XX AAO26678;
AC AAO26678;
XX 20-MAR-2003 (first entry)
XX
DE Human KIM-1 mucin domain protein, SEQ ID No 6.
XX
KW Cytostatic; gene therapy; antibody; antigen; antigen-binding;
KW proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;
KW renal disease; injury; renal cancer; human.
XX
OS Homo sapiens.
XX
PN WO200298920-A1.
XX
PD 12-DEC-2002.
XX
PF 31-MAY-2002; 2002WO-US017402.
XX
PR 01-JUN-2001; 2001US-0295449P.
PR 04-JUN-2001; 2001US-0295907P.
XX
PA (BIOJ) BIOGEN INC.
XX (GHEO) GEN HOSPITAL CORP.
XX
PI Bailly V, Bonventre J;
XX
DR WPI; 2003-156845/15.
XX
PT New antibody, antibody derivative or antigen-binding polypeptide that
PT inhibits proteolytic release of a soluble kidney injury molecule-1
PT polypeptide, useful for treating or preventing renal disease or injury,
PT e.g. renal cancer.
XX
PS Disclosure; Fig 1A; 42pp; English.
XX
CC The invention relates to a novel antibody, antibody derivative or antigen
CC -binding polypeptide that inhibits proteolytic release of a soluble
CC kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.
CC The antibody, antibody derivative or antigen-binding polypeptide is
CC useful for treating or preventing renal disease or injury, e.g. renal
CC cancer. The antibody is also useful for inhibiting shedding of the KIM-1
CC polypeptide. This sequence represents a human KIM-1 mucin domain protein
CC of the invention

SQ Sequence 81 AA;

Query Match 100.0%; Score 225; DB 6; Length 81;
 Best Local Similarity 100.0%; Pred. No. 3.3e-21;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLYSYTTDNDVTSSDGLWNNNTQLFLEHSLTANTTKG 42
 |||||
 DB 40 PLYSYTTDNDVTSSDGLWNNNTQLFLEHSLTANTTKG 81

RESULT 2

ADQ76693
 ID ADQ76693 standard; protein; 298 AA.

XX AC ADQ76693;

XX DT 07-OCT-2004 (first entry)

XX DE Human KIM-1 extracellular domain-6xHis fusion.

XX KW Human; KIM-1; kidney injury module-1; immunosuppressive; protozoacide;
 KW muscular-gen.; neuroprotective; antianaemic; antithyroid; haemostatic;
 KW antiallergic; antiinflammatory; vasotropic; nephrotropic.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Peptide 1..20
 /label= Signal_peptide

XX FT

XX PN WO2004060041-A2.

XX PD 22-JUL-2004.

XX PF 29-DEC-2003; 2003WO-US041294.

XX PR 30-DEC-2002; 2002US-0436934P.

XX PA (BIOG-) BIOGEN IDEC MA INC.

XX PI Rennert PD;

XX XX WPI; 2004-534277/51.

XX PT Use of a kidney injury molecule-1 (KIM-1) antagonist for e.g. treating
 PT Th2 cell-mediated diseases or inflammatory diseases, inhibiting B cell
 PT activation, or inhibiting production of a subset of antibodies against
 PT one or more antigens.

XX PS Example 3; Page 33; 68pp; English.

XX CC The present sequence is that of a polypeptide comprising the
 CC extracellular domain (residues 1-290) of human kidney injury molecule-1
 CC (KIM-1) ADQ76690 fused to a C-terminal 6xHis tag peptide. A plasmid
 CC comprising DNA encoding this sequence under control of a CMV promoter was
 CC used for transient constitutive expression of the polypeptide in
 CC mammalian cells in an example from the invention. The invention provides
 CC methods for therapeutically modulating immune function in autoimmune
 CC diseases and other disorders of the mammalian immune system. A method is
 CC claimed for inhibiting signalling between a T cell and a second cell,
 CC e.g. an antigen-presenting cell, in a mammal. The method involves
 CC identifying a mammal with an immune disease or disorder, or one preparing
 CC to receive a tissue graft, and administering a KIM-1 antagonist,
 CC especially a polypeptide comprising: a KIM-1 Ig domain, and lacking a
 CC transmembrane domain and a KIM-1 cytoplasmic domain; an anti-KIM-1
 CC antibody; or an antigen-binding fragment of an anti-KIM-1 antibody.
 CC Preferably, the KIM-1 antagonist is a soluble polypeptide, which can
 CC include a KIM-1 mucin domain in addition to the KIM Ig domain, and may
 CC include a heterologous moiety such as an Fc moiety. The antagonist may be
 CC conjugated to a polymer such as polyethylene glycol. The KIM-1 antagonist
 CC is used in methods of: inhibiting activation of a B cell in a mammal;

CC inhibiting disease relapse in an autoimmune disease; inhibiting epitope
 CC spreading in an autoimmune disease; treating a Th2 cell-mediated disease
 CC (e.g. myasthenia gravis, autoimmune haemolytic anaemia, Chagas disease,
 CC Grave's disease, idiopathic thrombocytopenia purpura, Wegener's
 CC granulomatosis, polyarteritis nodosa, rapidly progressive crescentic
 CC glomerulonephritis, graft-versus-host disease, or systemic lupus
 CC nephritis) or inflammatory disease or disorder (e.g. inflammatory bowel
 CC diseases such as Crohn's disease, ulcerative colitis, and ileitis); and
 CC inhibiting secretion of IFN-gamma by lymphocytes.

XX SQ Sequence 298 AA;

Query Match 100.0%; Score 225; DB 8; Length 298;
 Best Local Similarity 100.0%; Pred. No. 1.6e-20;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLYSYTTDNDVTSSDGLWNNNTQLFLEHSLTANTTKG 42
 |||||
 DB 249 PLYSYTTDNDVTSSDGLWNNNTQLFLEHSLTANTTKG 290

RESULT 3

AAW38336
 ID AAW38336 standard; protein; 334 AA.

XX AC AAW38336;

XX DT 21-MAY-1998 (first entry)

XX DE Human kidney injury related molecule (KIM).

XX KW Kidney injury related molecule; KIM; human; renal disease; injury;
 KW nephritis; tissue regeneration; therapy; monoclonal antibody.

XX OS Homo sapiens.

XX PN WO9744460-A1.

XX PD 27-NOV-1997.

XX PF 23-MAY-1997; 97WO-US009303.

XX PR 24-MAY-1996; 96US-0018228P.

XX PR 23-AUG-1996; 96US-0023442P.

XX PA (BIOJ) BIOGEN INC.

XX PI Sanicola-Nadel M, Bonventre JV, Hession CA, Ichimura T, Wei H;
 PI Cate RL;

XX DR WPI; 1998-018514/02.

XX PT DNA encoding kidney injury related molecule - which is upregulated in
 PT injured or regenerating tissue, useful to promote growth of new tissue
 PT and survival of damaged tissue.

XX PS Claim 9; Page 46-47; 68pp; English.

XX CC This protein, designated kidney injury related molecule (KIM), is up-
 CC regulated in injured or regenerating tissue. Its amino acid sequence was
 CC deduced from a clone (see AAT96035) obtained from a human embryonic liver
 CC library. A 572-amino acid (see AAW38335) and a 307-amino acid rat KIM
 CC (see AAW38334) are also claimed. Recombinant KIM polypeptides can be
 CC expressed in prokaryotic and eukaryotic host cells using a claimed
 CC process. Soluble variants fused to a toxin, imageable compound or
 CC radionuclide, and IgG fusion proteins are also claimed. KIM, or an
 CC agonist, can be used to treat renal disease and to promote the growth of new
 CC tissue or the survival of damaged tissue, generally in conditions where
 CC the binding of specific ligand to KIM stimulates cell growth, maintains
 CC cellular differentiation or reduces apoptosis, e.g. in cases of renal
 CC failure, nephritis, kidney transplants, toxic or hypoxic injury. A
 CC monoclonal antibody specific for KIM can be used to treat renal disease,
 CC e.g. where binding of KIM to ligand results in neoplasia, loss of

CC cellular function, susceptibility to apoptosis or promotion of
 CC inflammation, deliver imaging agents to KIM expressing cells in vivo or
 CC in vitro and measure KIM concentration by immunoassay.
 CC Damage/regeneration of renal cells can be determined by measuring KIM,
 CC particularly to diagnose or monitor the progress of disease or therapy.
 CC KIM-expressing tumour cells can be inhibited by treatment with a fusion
 CC protein comprising KIM ligand or Mab with a toxin or radionuclide, and
 CC tumour cells that express KIM ligand can be inhibited with similarly
 CC tagged KIM or anti-KIM ligand antibody
 XX
 SQ Sequence 334 AA;

Query Match 100.0%; Score 225; DB 2; Length 334;
 Best Local Similarity 100.0%; Pred. No. 1.9e-20;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSYTTDGNQDVTSSDGLWNNQTLFLEHSLLTANTTKG 42
 |||||
 Db 249 PLSYTTDGNQDVTSSDGLWNNQTLFLEHSLLTANTTKG 290
 |||||

RESULT 4
 ID AAO26679 standard; protein; 334 AA.
 XX
 AC AAO26679;
 XX
 DT 20-MAR-2003 (first entry)
 XX
 DE KIM-1 related protein, SEQ ID NO 7.
 XX
 KW Cytostatic; gene therapy; antibody; antigen; antigen-binding;
 XX proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;
 KW renal disease; injury; renal cancer; human.
 XX
 OS Homo sapiens.
 XX
 XN WO200298920-A1.
 XX
 PD 12-DEC-2002.
 XX
 PF 31-MAY-2002; 2002WO-US017402.
 XX
 PR 01-JUN-2001; 2001US-0295449P.
 XX 04-JUN-2001; 2001US-0295907P.
 XX
 PA (BIOJ) BIOGEN INC.
 XX (GEO) GEN HOSPITAL CORP.
 XX
 PI Bailey V, Bonventre J;
 XX
 DR WPI; 2003-156845/15.
 XX
 PT New antibody, antibody derivative or antigen-binding polypeptide that
 PT inhibits proteolytic release of a soluble kidney injury molecule-1
 PT polypeptide, useful for treating or preventing renal disease or injury,
 PT e.g. renal cancer.
 XX
 PS Disclosure; Page 39-40; 42pp; English.

CC The invention relates to a novel antibody, antibody derivative or antigen
 CC -binding polypeptide that inhibits proteolytic release of a soluble
 CC kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.
 CC The antibody, antibody derivative or antigen-binding polypeptide is
 CC useful for treating or preventing renal disease or injury, e.g. renal
 CC cancer. The antibody is also useful for inhibiting shedding of the KIM-1
 CC polypeptide. This sequence represents a protein relating to the KIM-1
 CC protein of the invention
 XX
 SQ Sequence 334 AA;

Query Match 100.0%; Score 225; DB 6; Length 334;
 Best Local Similarity 100.0%; Pred. No. 1.9e-20;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSYTTDGNQDVTSSDGLWNNQTLFLEHSLLTANTTKG 42
 |||||
 Db 249 PLSYTTDGNQDVTSSDGLWNNQTLFLEHSLLTANTTKG 290
 |||||

RESULT 5
 ID ADQ76696 standard; protein; 334 AA.
 XX
 AC ADQ76696;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Human kidney injury molecule-1 (KIM-1).
 XX
 KW Human; KIM-1; kidney injury molecule-1; immunosuppressive; protozoacide;
 KW muscular-gen.; neuroprotective; antianaemic; antithyroid; haemostatic;
 KW antiallergic; antiinflammatory; vasotropic; nephrotropic.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT Peptide I..20
 FT Modified-site /label= Signal_peptide
 FT Modified-site 65..67
 FT Modified-site /note= "N-glycosylated"
 FT Modified-site 258..260
 FT Modified-site /note= "N-glycosylated"
 FT Modified-site 272..274
 FT Modified-site /note= "N-glycosylated"
 FT Modified-site 286..288
 FT Modified-site /note= "N-glycosylated"
 FT Domain 290..311
 FT Region /note= "Transmembrane domain"
 FT Region 324..334
 FT /note= "C-terminal region unique to this splice variant"
 XX
 PN WO2004060041-A2.
 XX
 PD 22-JUL-2004.
 XX
 PF 29-DEC-2003; 2003WO-US041294.
 XX
 PR 30-DEC-2002; 2002US-0436934P.
 XX
 PA (BIOG-) BIOGEN IDEC MA INC.
 XX
 PI Rennert PD;
 XX
 DR WPI; 2004-534277/51.
 XX
 PT Use of a kidney injury molecule-1 (KIM-1) antagonist for e.g. treating
 PT Th2 cell-mediated diseases or inflammatory diseases, inhibiting B cell
 PT activation, or inhibiting production of a subset of antibodies against
 PT one or more antigens.
 XX
 PS Disclosure; SEQ ID NO 1; 68pp; English.

CC The present sequence is that of human kidney injury molecule-1 (KIM-1), a
 CC type I cell membrane glycoprotein and member of the T cell immunoglobulin
 CC (Ig) and mucin domain (TIM) family. This protein has 334 amino acids or
 CC 359 amino acids ADQ76690, depending on splice variation. It has been
 CC discovered that treatment of a mammal with a KIM-1 antagonist alters the
 CC interaction of T cells and other immune system cells, e.g. dendritic
 CC cells, monocytes, macrophages and B cells, and thereby strongly
 CC suppresses an IgG response to an antigen. Such treatment also eliminates
 CC IgG1 production by memory B cells in response to subsequent challenge
 CC with the antigen. Blockage of the binding of KIM-1 to its receptor
 CC reduces secretion of interferon-gamma by immune cells engaged in an
 CC antigen response in the mixed lymphocyte response assay. Based on these
 CC discoveries, the invention provides methods for therapeutically

modulating immune function in autoimmune diseases and other disorders of the mammalian immune system. A method is claimed for inhibiting signalling between a T cell and a second cell, e.g. an antigen-presenting cell, in a mammal. The method involves identifying a mammal with an immune disease or disorder, or one preparing to receive a tissue graft, and administering a KIM-1 antagonist, especially a polypeptide comprising: a KIM-1 Ig domain, and lacking a transmembrane domain and a KIM-1 cytoplasmic domain; an anti-KIM-1 antibody; or an antigen-binding fragment of an anti-KIM-1 antibody. Preferably, the KIM-1 antagonist is a soluble polypeptide, which can include a KIM-1 mucin domain in addition to the KIM Ig domain, and may include a heterologous moiety such as an Fc moiety. The antagonist may be conjugated to a polymer such as polyethylene glycol. The KIM-1 antagonist is used in methods of: inhibiting activation of a B cell in a mammal; inhibiting disease relapse in an autoimmune disease; inhibiting epitope spreading in an autoimmune disease; treating a Th2 cell-mediated disease (e.g. myasthenia gravis, autoimmune haemolytic anaemia, Chagas disease, Grave's disease, idiopathic thrombocytopenia purpura, Wegener's granulomatosis, polyarteritis nodosa, rapidly progressive crescentic glomerulonephritis, graft-versus-host disease, or systemic lupus nephritis) or inflammatory disease or disorder (e.g. inflammatory bowel diseases such as Crohn's disease, ulcerative colitis, and ileitis); and inhibiting secretion of IFN-gamma by lymphocytes.

Sequence 334 AA;
Query Match 100.0%; Score 225; DB 8; Length 334;
Best Local Similarity 100.0%; Pred. No. 1.9e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLYSYTTDGNVTVESSDGLWNNNTQLFLEHSLLTANTTKG 42
|||||
DB 249 PLYSYTTDGNVTVESSDGLWNNNTQLFLEHSLLTANTTKG 290

RESULT 6
ADE36618
ID ADE36618 standard; protein; 339 AA.
XX ADE36618;
AC ADE36618;
XX
XX 29-JAN-2004 (first entry)
DE Plasmid pCR2.1-CG57008-03-S843 15B protein insert SEQ ID NO:28.
XX human; NOVX; cytostatic; antiinflammatory; gene therapy; vaccine;
KW renal cancer; inflammation; tissue typing.
XX Synthetic.
OS Homo sapiens.
XX WO2003080856-A2.
FN
XX
XX 02-OCT-2003.
PD
PF 19-MAR-2003; 2003WO-US008490.
XX
XX 19-MAR-2002; 2002US-0365491P.
PR 13-SEP-2002; 2002US-0410618P.
XX
XX (CURA-) CURAGEN CORP.
PA
XX
XX Lepley DM, Rieger DK, Tse K, Rastelli L, Smithson G, Meeri M;
PI Ooi CE, Anderson DW, Guo X, Giot L, Starling G;
XX
XX WPI; 2003-876927/81.
DR N-PSDB; ADE36617.
XX
XX New polypeptide, useful for preparing a composition for treating or
PT preventing a pathology associated with NOVX polypeptide e.g. renal cancer
PT or inflammation, or for tissue typing.
XX
XX Example 1; SEQ ID NO 28; 239pp; English.

XX The present invention describes an isolated human NOVX polypeptide, where
CC X is 1a to 1d or 2a to 2h, or its mature form, a sequence that is at
CC least 95 % identical to it, or a sequence comprising one or more
CC conservative substitutions in the amino acid sequence. The NOVX
CC polypeptide, and nucleic acid sequence encoding it, has cytostatic and
CC antiinflammatory activities, and can be used in gene therapy, and in
CC vaccines. The NOVX polypeptide is useful for preparing a composition for
CC treating or preventing a pathology associated with NOVX polypeptide e.g.
CC renal cancer or inflammation, or for tissue typing. The present sequence
CC represents a pCR2.1-CG57008-03-S843 15B protein insert, which is used in
XX an example from the present invention.

Sequence 339 AA;
Query Match 100.0%; Score 225; DB 7; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.9e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLYSYTTDGNVTVESSDGLWNNNTQLFLEHSLLTANTTKG 42
|||||
DB 229 PLYSYTTDGNVTVESSDGLWNNNTQLFLEHSLLTANTTKG 270

RESULT 7
ADE36592
ID ADE36592 standard; protein; 339 AA.
XX
XX ADE36592;
AC
XX 29-JAN-2004 (first entry)
DT Human NOV1a protein SEQ ID NO:2.
DE
XX human; NOVX; cytostatic; antiinflammatory; gene therapy; vaccine;
KW renal cancer; inflammation; tissue typing.
XX Homo sapiens.
OS WO2003080856-A2.
XX
XX 02-OCT-2003.
PD
PF 19-MAR-2003; 2003WO-US008490.
XX
XX 19-MAR-2002; 2002US-0365491P.
PR 13-SEP-2002; 2002US-0410618P.
XX
XX (CURA-) CURAGEN CORP.
PA
XX
XX Lepley DM, Rieger DK, Tse K, Rastelli L, Smithson G, Meeri M;
PI Ooi CE, Anderson DW, Guo X, Giot L, Starling G;
XX
XX WPI; 2003-876927/81.
DR N-PSDB; ADE36591.
XX
XX New polypeptide, useful for preparing a composition for treating or
PT preventing a pathology associated with NOVX polypeptide e.g. renal cancer
PT or inflammation, or for tissue typing.
XX
XX Claim 1; SEQ ID NO 2; 239pp; English.

XX The present invention describes an isolated human NOVX polypeptide, where
CC X is 1a to 1d or 2a to 2h, or its mature form, a sequence that is at
CC least 95 % identical to it, or a sequence comprising one or more
CC conservative substitutions in the amino acid sequence. The NOVX
CC polypeptide, and nucleic acid sequence encoding it, has cytostatic and
CC antiinflammatory activities, and can be used in gene therapy, and in
CC vaccines. The NOVX polypeptide is useful for preparing a composition for
CC treating or preventing a pathology associated with NOVX polypeptide e.g.
CC renal cancer or inflammation, or for tissue typing. The present sequence
CC represents human NOV1a from the present invention.

SQ	Sequence 339 AA;	
Query Match	100.0%; Score 225; DB 7; Length 339;	
Best Local Similarity	100.0%; Pred. No. 1.9e-20;	
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 PLYSVTTDGNVTWTESSDGLWNNQTLFLEHSLLTANTTKG 42	
DB	229 PLYSVTTDGNVTWTESSDGLWNNQTLFLEHSLLTANTTKG 270	
RESULT 8		
ABR58582		
ID	ABR58582 standard; protein; 359 AA.	
XX		
AC	ABR58582;	
DT	09-JUL-2003 (first entry)	
XX		
DE	Human cancer related protein SEQ ID NO:239.	
XX		
KW	Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;	
KW	heart disease; atherosclerosis; endometriosis.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2003025138-A2.	
XX		
PD	27-MAR-2003.	
XX		
PF	17-SEP-2002; 2002WO-US029560.	
XX		
PR	17-SEP-2001; 2001US-0323469P.	
PR	20-SEP-2001; 2001US-0323887P.	
PR	13-NOV-2001; 2001US-0350666P.	
PR	08-FEB-2002; 2002US-0355145P.	
PR	08-FEB-2002; 2002US-0355257P.	
PR	12-APR-2002; 2002US-0372246P.	
XX		
PA	(EOSB-) EOS BIOTECHNOLOGY INC.	
XX		
PI	Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;	
PI	Zlotnik A;	
XX		
DR	WPI; 2003-354600/33.	
DR	N-PSDB; ACC72709.	
XX		
PT	New genes that are up-regulated or down-regulated in cancers, useful as	
PT	markers for diagnosing e.g. cancer, ischemia or heart diseases, or as	
PT	therapeutic targets for screening drugs for treating these diseases.	
XX		
PS	Claim 12; Page 742; 767pp; English.	
XX		
CC	The present invention describes an isolated nucleic acid molecule, which	
CC	comprises the sequence of any of the genes that are up-regulated or down-	
CC	regulated in specific cancers (e.g. about 1031 genes up-regulated in	
CC	acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer	
CC	related gene nucleotide sequences which encode the proteins given in	
CC	ABR58521 to ABR58709. Also described: (1) determining the presence or	
CC	absence of a pathological cell in a patient; (2) an expression vector	
CC	comprising a nucleic acid molecule described above; (3) a host cell	
CC	comprising the vector; (4) an isolated polypeptide, which is encoded by	
CC	the nucleic acid; (5) an antibody that specifically binds the polypeptide	
CC	of (4); (6) specifically targeting a compound to a pathological cell in a	
CC	patient by administering to the patient the antibody above; and (7) a	
CC	drug screening assay. The nucleic acid is useful as diagnostic markers or	
CC	therapeutic targets. In particular, the nucleic acid is useful for	
CC	diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,	
CC	bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,	
CC	pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,	
CC	atherosclerosis and endometriosis. The nucleic acid is also useful in	
CC	drug screening, particularly for identifying agents for treating these	
CC	pathologies	

XX	Sequence 359 AA;	
Query Match	100.0%; Score 225; DB 6; Length 359;	
Best Local Similarity	100.0%; Pred. No. 2e-20;	
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 PLYSVTTDGNVTWTESSDGLWNNQTLFLEHSLLTANTTKG 42	
DB	249 PLYSVTTDGNVTWTESSDGLWNNQTLFLEHSLLTANTTKG 290	
RESULT 9		
ABP70439		
ID	ABP70439 standard; protein; 359 AA.	
XX		
AC	ABP70439;	
DT	22-APR-2003 (first entry)	
XX		
DE	Amino acid sequence of human TIM-1 allele 1.	
XX		
KW	T cell immunoglobulin domain; mucin domain; TIM; TIM-1; TIM-2; TIM-3;	
KW	TIM-4; immune dysfunction; chromosome 5; malignancy; allergy; eczema;	
KW	myelodysplastic syndrome; airway hyperreactivity; cancer; asthma;	
KW	allergic T cell response; autoimmune disease.	
OS	Homo sapiens.	
XX		
PN	WO2003002722-A2.	
XX		
PD	09-JAN-2003.	
XX		
PF	01-JUL-2002; 2002WO-US020890.	
XX		
PR	29-JUN-2001; 2001US-0302344P.	
XX		
PA	(STRD) UNIV LELAND STANFORD JUNIOR.	
XX		
PI	McIntire JJ, Dekruff RH, Umetsu DT, Freeman GJ, Kuchroo V;	
PI	WPI; 2003-210268/20.	
DR	N-PSDB; ABZ68333.	
XX		
PT	New nucleic acid comprising a mammalian T cell immunoglobulin domain and	
PT	Mucin domain gene sequences, useful for treating cancer or asthma,	
PT	allergy, eczema or autoimmune disease.	
XX		
PS	Claim 10; Page 82; 94pp; English.	
XX		
CC	The present sequence is a human T cell immunoglobulin domain and mucin	
CC	domain-1 (TIM-1) polypeptide. The specification describes TIM-1, TIM-2,	
CC	TIM-3 and TIM-4. TIM polypeptides are cell surface molecules with	
CC	conserved IgV and mucin domains. The locus comprising the TIM family is	
CC	genetically associated with immune dysfunction, including asthma. The TIM	
CC	gene family is located within a region of human chromosome 5 that is	
CC	commonly deleted in malignancies and myelodysplastic syndrome. Variants	
CC	of TIM-1 and TIM-3 are associated with susceptibility to airway	
CC	hyperactivity and allergic T cell responses, and other variants	
CC	associated with protection against these responses. T cells express TIM	
CC	proteins, which critically regulate CD4 T cell differentiation. Th1 cells	
CC	preferentially express TIM-3, while Th2 cells preferentially express TIM-	
CC	1. TIM polypeptides and polynucleotides are useful for treating cancer,	
CC	asthma, allergies, eczema or autoimmune diseases	
XX		
SQ	Sequence 359 AA;	
Query Match	100.0%; Score 225; DB 6; Length 359;	
Best Local Similarity	100.0%; Pred. No. 2e-20;	
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 PLYSVTTDGNVTWTESSDGLWNNQTLFLEHSLLTANTTKG 42	
DB	249 PLYSVTTDGNVTWTESSDGLWNNQTLFLEHSLLTANTTKG 290	

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Db      249 PLYSYTGDNDVTVESSDGLMNNQTLFLEHSLLTANTTKG 290
RESULT 10
ID      ABP70438
XX      Human bladder cancer associated protein sequence SEQ ID NO:64.
XX      Human; bladder cancer; cytostatic; gene therapy; vaccine.
AC      ABP70438;
XX      Homo sapiens.
DT      22-APR-2003 (first entry)
XX      WO2003003906-A2.
DE      16-JAN-2003.
XX      03-JUL-2002; 2002WO-US021338.
KW      T cell immunoglobulin domain; mucin domain; TIM; TIM-1; TIM-2; TIM-3;
KW      TIM-4; immune dysfunction; chromosome 5; malignancy; allergy; eczema;
KW      myelodysplastic syndrome; airway hyperreactivity; cancer; asthma;
KW      allergic T cell response; autoimmune disease.
OS      Homo sapiens.
XX      WO2003002722-A2.
FN      09-JAN-2003.
PD      01-JUL-2002; 2002WO-US020890.
PF      29-JUN-2001; 2001US-0302344P.
XX      (STRD ) UNIV LELAND STANFORD JUNIOR.
PA      McIntire JJ, Dekruyff RH, Umetsu DT, Freeman GJ, Kuchroo V;
XX      WPI; 2003-210268/20.
DR      N-PSDB; ABZ68332.
XX      New nucleic acid comprising a mammalian T cell immunoglobulin domain and
PT      Mucin domain gene sequences, useful for treating cancer or asthma,
PT      allergy, eczema or autoimmune disease.
XX      Claim 10; Page 80-81; 94pp; English.
PS      The present sequence is a human T cell immunoglobulin domain and mucin
XX      domain-1 (TIM-1) polypeptide. The specification describes TIM-1, TIM-2,
CC      TIM-3 and TIM-4. TIM polypeptides are cell surface molecules with
CC      conserved IGV and mucin domains. The locus comprising the TIM family is
CC      genetically associated with immune dysfunction, including asthma. The TIM
CC      gene family is located within a region of human chromosome 5 that is
CC      commonly deleted in malignancies and myelodysplastic syndrome. Variants
CC      of TIM-1 and TIM-3 are associated with susceptibility to airway
CC      hyperactivity and allergic T cell responses, and other variants
CC      associated with protection against these responses. T cells express TIM
CC      proteins, which critically regulate CD4 T cell differentiation. Th1 cells
CC      preferentially express TIM-3, while Th2 cells preferentially express TIM-
CC      1. TIM polypeptides and polynucleotides are useful for treating cancer,
CC      asthma, allergies, eczema or autoimmune diseases
XX      Sequence 359 AA;
SQ      Query Match      100.0%; Score 225; DB 6; Length 359;
      Best Local Similarity 100.0%; Pred. No. 2e-20;
      Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PLYSYTGDNDVTVESSDGLMNNQTLFLEHSLLTANTTKG 42
      |||||
DB      249 PLYSYTGDNDVTVESSDGLMNNQTLFLEHSLLTANTTKG 290
      |||||

RESULT 12
ID      AAO26680
XX      AAO26680 standard; protein; 359 AA.
XX      AAO26680;
AC      AAO26680;
XX      20-MAR-2003 (first entry)
DT      KIM-1 related protein, SEQ ID No 8.
XX      Cytostatic; gene therapy; antibody; antigen; antigen-binding;
XX      proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;
XX      renal disease; injury; renal cancer; human.
KW

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XX Homo sapiens.
OS WO200298920-A1.
PN
XX
XX
PD 12-DEC-2002.
XX
XX 31-MAY-2002; 2002WO-US017402.
PF
XX 01-JUN-2001; 2001US-0295449P.
XX 04-JUN-2001; 2001US-0295907P.
PR
XX (BIOJ) BIOGEN INC.
PA (GEHO) GEN HOSPITAL CORP.
XX
XX Baillly V, Bonventre J;
XX WPI; 2003-156845/15.
DR
XX New antibody, antibody derivative or antigen-binding polypeptide that
PT inhibits proteolytic release of a soluble kidney injury molecule-1
PT polypeptide, useful for treating or preventing renal disease or injury,
PT e.g. renal cancer.
XX
XX Disclosure; Page 40-41; 42pp; English.
XX
XX The invention relates to a novel antibody, antibody derivative or antigen
CC -binding polypeptide that inhibits proteolytic release of a soluble
CC kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.
CC The antibody, antibody derivative or antigen-binding polypeptide is
CC useful for treating or preventing renal disease or injury, e.g. renal
CC cancer. The antibody is also useful for inhibiting shedding of the KIM-1
CC polypeptide. This sequence represents a protein relating to the KIM-1
CC protein of the invention
XX
XX Sequence 359 AA;
SQ
Query Match 100.0%; Score 225; DB 6; Length 359;
Best Local Similarity 100.0%; Pred. No. 2e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 PLYSYTDCNDVTSSDGLWNNQQLFLEHSLLTANTTKG 42
DB 249 PLYSYTDCNDVTSSDGLWNNQQLFLEHSLLTANTTKG 290
RESULT 13
ADE36594
ID ADE36594 standard; protein; 359 AA.
XX
XX ADE36594;
AC
XX 29-JAN-2004 (first entry)
DT
XX Human NOV1b protein SEQ ID NO:4.
DE
XX human; NOVX; cytostatic; antiinflammatory; gene therapy; vaccine;
KW renal cancer; inflammation; tissue typing.
XX
XX Homo sapiens.
OS
XX WO2003080856-A2.
PN
XX 02-OCT-2003.
XX
XX 19-MAR-2003; 2003WO-US008490.
PF
XX 19-MAR-2002; 2002US-0365491P.
XX
XX 13-SEP-2002; 2002US-0410618P.
PR
XX (CURA-) CURAGEN CORP.
PA
XX
XX Lepley DW, Rieger DK, Tse K, Rastelli L, Smithson G, Mesri M;

PI Ooi CE, Anderson DW, Guo X, Giot L, Starling G;
XX WPI; 2003-876927/81.
DR N-PSDB; ADE36593.
XX
XX New polypeptide, useful for preparing a composition for treating or
PT preventing a pathology associated with NOVX polypeptide e.g. renal cancer
PT or inflammation, or for tissue typing.
XX
XX Claim 1; SEQ ID NO 4; 239pp; English.
PS
XX The present invention describes an isolated human NOVX polypeptide, where
CC X is la to ld or 2a to 2h, or its mature form, a sequence that is at
CC least 95 % identical to it, or a sequence comprising one or more
CC conservative substitutions in the amino acid sequence. The NOVX
CC polypeptide, and nucleic acid sequence encoding it, has cytostatic and
CC antiinflammatory activities, and can be used in gene therapy, and in
CC vaccines. The NOVX polypeptide is useful for preparing a composition for
CC treating or preventing a pathology associated with NOVX polypeptide e.g.
CC renal cancer or inflammation, or for tissue typing. The present sequence
CC represents human NOV1b from the present invention.
XX
XX Sequence 359 AA;
SQ
Query Match 100.0%; Score 225; DB 7; Length 359;
Best Local Similarity 100.0%; Pred. No. 2e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 PLYSYTDCNDVTSSDGLWNNQQLFLEHSLLTANTTKG 42
DB 249 PLYSYTDCNDVTSSDGLWNNQQLFLEHSLLTANTTKG 290
RESULT 14
ADN38984
ID ADN38984 standard; protein; 359 AA.
XX
XX ADN38984;
AC
XX 17-JUN-2004 (first entry)
DT
XX Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:302.
DE
XX Human; differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW retinal neovascularisation syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW vulneryary; gene therapy; vaccine.
XX
XX Homo sapiens.
OS
XX WO2003042661-A2.
PN
XX 22-MAY-2003.
PD
XX 13-NOV-2002; 2002WO-US036810.
PF
XX 13-NOV-2001; 2001US-0350666P.
XX 21-NOV-2001; 2001US-0332464P.
PR 29-NOV-2001; 2001US-0334393P.
PR 03-DEC-2001; 2001US-0335394P.
PR 14-DEC-2001; 2001US-0340376P.
PR 08-JAN-2002; 2002US-0347211P.
PR 10-JAN-2002; 2002US-0347349P.
PR 08-FEB-2002; 2002US-0355250P.
PR 13-FEB-2002; 2002US-0356714P.
PR 20-FEB-2002; 2002US-0359077P.
PR 29-MAR-2002; 2002US-0368809P.
PR 04-APR-2002; 2002US-0370110P.
PR 12-APR-2002; 2002US-0372246P.
PR 05-JUN-2002; 2002US-0386614P.

PR 16-JUL-2002; 2002US-0396839P.
PR 22-JUL-2002; 2002US-0397775P.
PR 22-JUL-2002; 2002US-0397845P.
PR 09-SEP-2002; 2002US-0409450P.
XX
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX
XX WPI; 2003-468649/44.
DR N-PSDB; ADN38983.
XX
XX Determining the presence or absence of a pathological cell in a patient,
PT useful for diagnosing, prognosing or treating cancer, comprises detecting
PT a nucleic acid in a biological sample.
XX
XX Claim 12; SEQ ID NO 302; 1385pp; English.
XX
XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularisation syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a polypeptide of the invention.
XX
SQ Sequence 359 AA;

Query Match 100.0%; Score 225; DB 7; Length 359;
Best Local Similarity 100.0%; Pred. No. 2e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLYSYTGDNDVTVESSDGLWNNNTQQLFLEHSLLTANTTKG 42
|||||
Db 249 PLYSYTGDNDVTVESSDGLWNNNTQQLFLEHSLLTANTTKG 290

RESULT 15
ADQ76690
ID ADQ76690 standard; protein; 359 AA.

XX AC ADQ76690;

XX DT 16-DEC-2004 (first entry)

DE Human kidney injury molecule-1 (KIM-1).

XX Human; KIM-1; kidney injury molecule-1; immunosuppressive; protozoacide;
KW muscular-gen.; neuroprotective; antianaemic; antithyroid; haemostatic;
KW antiallergic; antiinflammatory; vasotropic; nephrotropic.
XX

OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..20

FT /label= Signal_peptide

FT Modified-site 65..67

FT /note= "N-glycosylated"

FT Modified-site 258..260

FT /note= "N-glycosylated"

FT Modified-site 272..274

FT /note= "N-glycosylated"

FT Modified-site 286..288
FT /note= "N-glycosylated"
FT Domain 290..311
FT /note= "Transmembrane domain"
FT Region 324..359
FT /note= "C-terminal region unique to this splice variant"
XX
XX WO2004060041-A2.
XX
XX 22-JUL-2004.
XX
XX 29-DEC-2003; 2003WO-US041294.
XX
XX 30-DEC-2002; 2002US-0436934P.
XX (BIOG-) BIOGEN IDEC MA INC.
XX
XX Rennett PD;
XX
XX WPI; 2004-534277/51.
XX
XX Use of a kidney injury molecule-1 (KIM-1) antagonist for e.g. treating
PT Th2 cell-mediated diseases or inflammatory diseases, inhibiting B cell
PT activation, or inhibiting production of a subset of antibodies against
PT one or more antigens.
XX
XX Disclosure; SEQ ID NO 1; 68pp; English.

XX The present sequence is that of human kidney injury molecule-1 (KIM-1), a
CC type I cell membrane glycoprotein and member of the T cell immunoglobulin
CC (Ig) and mucin domain (TIM) family. This protein has 334 amino acids
CC AD076696 or 359 amino acids, depending on splice variation. It has been
CC discovered that treatment of a mammal with a KIM-1 antagonist alters the
CC interaction of T cells and other immune system cells, e.g. dendritic
CC cells, monocytes, macrophages and B cells, and thereby strongly
CC suppresses an IgG response to an antigen. Such treatment also eliminates
CC IgG1 production by memory B cells in response to subsequent challenge
CC with the antigen. Blockage of the binding of KIM-1 to its receptor
CC reduces secretion of interferon-gamma by immune cells engaged in an
CC antigen response in the mixed lymphocyte response assay. Based on these
CC discoveries, the invention provides methods for therapeutically
CC modulating immune function in autoimmune diseases and other disorders of
CC the mammalian immune system. A method is claimed for inhibiting
CC signalling between a T cell and a second cell, e.g. an antigen-presenting
CC cell, in a mammal. The method involves identifying a mammal with an
CC immune disease or disorder, or one preparing to receive a tissue graft,
CC and administering a KIM-1 antagonist, especially a polypeptide
CC comprising: a KIM-1 Ig domain, and lacking a transmembrane domain and a
CC KIM-1 cytoplasmic domain; an anti-KIM-1 antibody; or an antigen-binding
CC fragment of an anti-KIM-1 antibody. Preferably, the KIM-1 antagonist is a
CC soluble polypeptide, which can include a KIM-1 mucin domain in addition
CC to the KIM Ig domain, and may include a heterologous moiety such as an Fc
CC moiety. The antagonist may be conjugated to a polymer such as
CC polyethylene glycol. The KIM-1 antagonist is used in methods of:
CC inhibiting activation of a B cell in a mammal; inhibiting in an autoimmune
CC in an autoimmune disease; inhibiting epitope spreading in an autoimmune
CC disease; treating a Th2 cell-mediated disease (e.g. myasthenia gravis,
CC autoimmune haemolytic anaemia, Chagas disease, Grave's disease,
CC idiopathic thrombocytopenia purpura, Wegener's granulomatosis,
CC polyarteritis nodosa, rapidly progressive crescentic glomerulonephritis,
CC graft-versus-host disease, or systemic lupus nephritis) or inflammatory
CC disease or disorder (e.g. inflammatory bowel diseases such as Crohn's
CC disease, ulcerative colitis, and ileitis); and inhibiting secretion of
CC IFN-gamma by lymphocytes.

XX SQ Sequence 359 AA;

Query Match 100.0%; Score 225; DB 8; Length 359;

Best Local Similarity 100.0%; Pred. No. 2e-20;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLYSYTGDNDVTVESSDGLWNNNTQQLFLEHSLLTANTTKG 42
|||||

Db 249 PLYSYTDCNDVTESDGLWNNNQTLFLEHSLLTANTTKG 290

Search completed: June 29, 2005, 09:09:07
Job time : 30.8703 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 08:57:16 ; Search time 5.77603 Seconds
(without alignments)
542.805 Million cell updates/sec

Title: US-10-718-321-6_COPY_40_81

Perfect score: 225

Sequence: 1 PLYSYTDCNDVTYESSDGL.....NNQTQLFLEHSLLTANTTKG 42

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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- 2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	225	100.0	334	4	US-09-197-970B-7
2	178	79.1	451	1	US-08-287-001A-2
3	178	79.1	451	5	PCT-US95-09941-2
4	60	26.7	602	1	US-08-168-091A-2
5	60	26.7	602	1	US-08-428-926-5
6	60	26.7	602	1	US-08-428-927-5
7	60	26.7	602	1	US-08-428-298-5
8	60	26.7	602	1	US-08-339-517-5
9	60	26.7	606	4	US-09-603-208A-56
10	60	26.7	1070	3	US-08-697-954-2
11	58	25.8	981	4	US-09-991-258-13
12	57	25.3	307	4	US-09-197-970B-3
13	54.5	24.2	323	6	5260223-4
14	54.5	24.2	323	6	5260223-4
15	53.5	23.8	10182	3	US-09-134-001C-3159
16	53	23.6	190	3	US-08-341-018-44
17	53	23.6	190	3	US-08-470-335-217
18	53	23.6	190	3	US-08-470-339-217
19	53	23.6	190	4	US-08-467-602-411
20	53	23.6	210	4	US-08-467-602-191
21	53	23.6	210	4	US-08-411-295F-315
22	53	23.6	213	4	US-08-467-602-186
23	53	23.6	213	4	US-08-411-295F-310
24	53	23.6	219	4	US-08-467-602-200
25	53	23.6	219	4	US-08-411-295F-324
26	53	23.6	222	4	US-08-467-602-197
27	53	23.6	222	4	US-08-411-295F-321

28	53	23.6	224	4	US-09-248-796A-18758	Sequence 18758, A
29	53	23.6	233	4	US-08-467-602-194	Sequence 194, App
30	53	23.6	233	4	US-08-411-295F-318	Sequence 318, App
31	53	23.6	242	4	US-08-467-602-203	Sequence 203, App
32	53	23.6	242	4	US-08-411-295F-327	Sequence 327, App
33	53	23.6	309	4	US-09-248-796A-25339	Sequence 25339, A
34	53	23.6	352	4	US-08-467-602-239	Sequence 239, App
35	53	23.6	352	4	US-08-411-295F-165	Sequence 165, App
36	53	23.6	355	4	US-08-467-602-234	Sequence 234, App
37	53	23.6	355	4	US-08-411-295F-160	Sequence 160, App
38	53	23.6	361	4	US-08-467-602-248	Sequence 248, App
39	53	23.6	361	4	US-08-411-295F-174	Sequence 174, App
40	53	23.6	364	4	US-08-467-602-245	Sequence 245, App
41	53	23.6	364	4	US-08-411-295F-171	Sequence 171, App
42	53	23.6	375	4	US-08-467-602-242	Sequence 242, App
43	53	23.6	375	4	US-08-411-295F-168	Sequence 168, App
44	53	23.6	384	4	US-08-467-602-251	Sequence 251, App
45	53	23.6	384	4	US-08-411-295F-177	Sequence 177, App

ALIGNMENTS

RESULT 1
US-09-197-970B-7
; Sequence 7, Application US/09197970B
; Patent No. 6664385
; GENERAL INFORMATION:
; APPLICANT: Michele Sanicola-Nadel
; Joseph V. Bonventre
; Catherine A. Hession
; Takaharu Ichimura
; Henry Wei
; Richard L. Cate
; TITLE OF INVENTION: MODULATORS OF TISSUE REGENERATION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/197,970B
; FILING DATE: 23-No. 6664385-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/018,228
; FILING DATE: 24-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Levine, Leslie M.
; REGISTRATION NUMBER: 35,245
; REFERENCE/DOCKET NUMBER: A010 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 679-2810
; TELEFAX: (617) 679-2838
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 334 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-197-970B-7
Query Match 100.0%; Score 225; DB 4; Length 334;
Best Local Similarity 100.0%; Pred. No. 2.8e-22;

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Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLYSYTGDNDVTSSDGLWNNNTQLFLEHSLLTANTTKG 42
Db 249 PLYSYTGDNDVTSSDGLWNNNTQLFLEHSLLTANTTKG 290

RESULT 2
US-08-287-001A-2
; Sequence 2, Application US/08287001A
; Patent No. 5622861
; GENERAL INFORMATION:
; APPLICANT: KAPLAN, GERARDO
; APPLICANT: FRINSTONE, STEPHEN M.
; TITLE OF INVENTION: HEPATITIS A VIRUS RECEPTOR AND METHODS
; TITLE OF INVENTION: OF USE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSER: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, The Candler Bldg, 127 Peachtree
; STREET: Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/287,001A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Spratt, Gwedolyn D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 1414.621
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-9880
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-001A-2

Query Match 79.1%; Score 178; DB 1; Length 451;
Best Local Similarity 81.0%; Pred. No. 8.8e-16;
Matches 34; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 PLYSYTGDNDVTSSDGLWNNNTQLFLEHSLLTANTTKG 42
Db 329 PLYSYTGDNDVTSSDGLWNNNTQLSPEHSPQWVNTTEG 370

RESULT 3
PCT-US95-09941-2
; Sequence 2, Application PC/TUS9509941
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HEPATITIS A VIRUS RECEPTOR AND METHODS
; TITLE OF INVENTION: OF USE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSER: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, The Candler Bldg, 127 Peachtree
; STREET: Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA

Query Match 79.1%; Score 178; DB 1; Length 451;
Best Local Similarity 81.0%; Pred. No. 8.8e-16;
Matches 34; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 PLYSYTGDNDVTSSDGLWNNNTQLFLEHSLLTANTTKG 42
Db 329 PLYSYTGDNDVTSSDGLWNNNTQLSPEHSPQWVNTTEG 370

RESULT 4
US-08-168-091A-2
; Sequence 2, Application US/08168091A
; Patent No. 5665862
; GENERAL INFORMATION:
; APPLICANT: Fischbach, Gerald.
; APPLICANT: Falls, Douglas R.
; APPLICANT: Rosen, Kenneth M.
; APPLICANT: Corfas, Gabriel
; TITLE OF INVENTION: Neurotrophic Factor
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LAHIVE AND COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/168,091A
; FILING DATE: 15-DEC-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/953,742
; FILING DATE: 29-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: HMI-002CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
```

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; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09941
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/287,001
; FILING DATE: 5 AUG 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Spratt, Gwedolyn D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 1414.621
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-09941-2

Query Match 79.1%; Score 178; DB 5; Length 451;
Best Local Similarity 81.0%; Pred. No. 8.8e-16;
Matches 34; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 PLYSYTGDNDVTSSDGLWNNNTQLFLEHSLLTANTTKG 42
Db 329 PLYSYTGDNDVTSSDGLWNNNTQLSPEHSPQWVNTTEG 370

RESULT 4
US-08-168-091A-2
; Sequence 2, Application US/08168091A
; Patent No. 5665862
; GENERAL INFORMATION:
; APPLICANT: Fischbach, Gerald.
; APPLICANT: Falls, Douglas R.
; APPLICANT: Rosen, Kenneth M.
; APPLICANT: Corfas, Gabriel
; TITLE OF INVENTION: Neurotrophic Factor
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LAHIVE AND COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/168,091A
; FILING DATE: 15-DEC-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/953,742
; FILING DATE: 29-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: HMI-002CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
```



```
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/339517
/ FILING DATE: 14-NOV-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lee, Wendy M.
/ REGISTRATION NUMBER: 00,000
/ REFERENCE/DOCKET NUMBER: 853D2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415/225-1994
/ TELEFAX: 415/952-9881
/ TELEX: 910/371-7168
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 602 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
US-08-428-298-5

Query Match 26.7%; Score 60; DB 1; Length 602;
Best Local Similarity 31.7%; Pred. No. 10;
Matches 13; Conservative 11; Mismatches 15; Indels 2; Gaps 1;

QY 3 YSYTGDNDVTYESSDGLWNNQTLFL--EHSLLTANTTK 41
Db 301 YTSHTHSMVTQTTPSHWSNGHTESILSESHSVLVSSSVE 341

RESULT 8
US-08-339-517-5
/ Sequence 5, Application US/08339517
/ Patent No. 5770567
/ GENERAL INFORMATION:
/ APPLICANT: Ho, Wei-Hsien
/ APPLICANT: Osheroff, Phyllis L.
/ TITLE OF INVENTION: SENSORY AND MOTOR NEURON DERIVED FACTOR (SMDF)
/ NUMBER OF SEQUENCES: 5
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genentech, Inc.
/ STREET: 460 Point San Bruno Blvd
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: patin (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/339,517
/ FILING DATE: 14-NOV-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lee, Wendy M.
/ REGISTRATION NUMBER: 00,000
/ REFERENCE/DOCKET NUMBER: 853
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415/225-1994
/ TELEFAX: 415/952-9881
/ TELEX: 910/371-7168
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 602 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
US-08-339-517-5

Query Match 26.7%; Score 60; DB 1; Length 602;
Best Local Similarity 31.7%; Pred. No. 10;
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Matches 13; Conservative 11; Mismatches 15; Indels 2; Gaps 1;

QY 3 YSYTGDNDVTYESSDGLWNNQTLFL--EHSLLTANTTK 41
Db 301 YTSHTHSMVTQTTPSHWSNGHTESILSESHSVLVSSSVE 341

RESULT 9
US-09-603-208A-56
/ Sequence 56, Application US/09603208A
/ Patent No. 6822084
/ GENERAL INFORMATION:
/ APPLICANT: Pompejus, Markus
/ APPLICANT: Kroger, Burkhard
/ APPLICANT: Schroder, Hartwig
/ APPLICANT: Zelder, Oskar
/ APPLICANT: Haberhauer, Gregor
/ APPLICANT: Lee, Heung-Shick
/ APPLICANT: Kim, Hyung-Joon
/ TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS,
/ TITLE OF INVENTION: RESISTANCE AND TOLERANCE PROTEINS
/ FILE REFERENCE: BGI-124CP
/ CURRENT APPLICATION NUMBER: US/09/603,208A
/ PRIOR FILING DATE: 2000-06-23
/ PRIOR APPLICATION NUMBER: 60/141031
/ PRIOR FILING DATE: 1999-06-25
/ PRIOR APPLICATION NUMBER: 60/142692
/ PRIOR FILING DATE: 1999-07-01
/ PRIOR APPLICATION NUMBER: 60/151214
/ PRIOR FILING DATE: 1999-08-27
/ PRIOR APPLICATION NUMBER: DE 19930429.7
/ PRIOR FILING DATE: 1999-07-01
/ PRIOR APPLICATION NUMBER: DE 19931413.6
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19931457.8
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19931541.8
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19932209.0
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: DE 19932230.9
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: DE 19932914.1
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: DE 19940764.9
/ PRIOR FILING DATE: 1999-08-27
/ PRIOR APPLICATION NUMBER: DE 19941382.7
/ PRIOR FILING DATE: 1999-08-31
/ NUMBER OF SEQ ID NOS: 306
/ SEQ ID NO 56
/ LENGTH: 606
/ TYPE: PRT
/ ORGANISM: Corynebacterium glutamicum
US-09-603-208A-56

Query Match 26.7%; Score 60; DB 4; Length 606;
Best Local Similarity 34.1%; Pred. No. 10;
Matches 14; Conservative 4; Mismatches 23; Indels 0; Gaps 0;

QY 1 PLYSYTGDNDVTYESSDGLWNNQTLFLSHLLTANTTK 41
Db 559 FLVEYQEGGDMFGMGKDIKEETVQLFLSASSSSSKTRK 599

RESULT 10
US-08-697-954-2
/ Sequence 2, Application US/08697954
/ Patent No. 6284535
/ GENERAL INFORMATION:
/ APPLICANT: Role, Lorna W.
/ TITLE OF INVENTION: SPLICE VARIANTS OF THE HEREGULIN GENE, PARIA, AND
/ TITLE OF INVENTION: USES THEREOF
/ NUMBER OF SEQUENCES: 4
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[illegible]

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 08:58:20 ; Search time 26.3222 Seconds
(without alignments)
613.589 Million cell updates/sec

Title: US-10-718-321-6_COPY_40_81

Perfect score: 225
Sequence: 1 PLYSVTTGNDVTWSSDGL.....NNQTQLEHSLLTANTTKG 42

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA.*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	225	100.0	81	17	US-10-718-321-6
2	225	100.0	334	17	US-10-655-506-7
3	225	100.0	334	17	US-10-718-321-7
4	225	100.0	339	17	US-10-391-939A-2
5	225	100.0	339	17	US-10-391-939A-28
6	225	100.0	359	14	US-10-188-012-17
7	225	100.0	359	14	US-10-188-012-19
8	225	100.0	359	15	US-10-295-027-302
9	225	100.0	359	15	US-10-188-832-64
10	225	100.0	359	17	US-10-391-939A-4
11	225	100.0	359	17	US-10-663-497-17
					Sequence 6, Appli
					Sequence 7, Appli
					Sequence 2, Appli
					Sequence 28, Appli
					Sequence 17, Appli
					Sequence 19, Appli
					Sequence 302, App
					Sequence 64, Appli
					Sequence 4, Appli
					Sequence 17, Appli

ALIGNMENTS

RESULT 1

US-10-718-321-6
; Sequence 6, Application US/10718321
; Publication NO. US20050112117A1
; GENERAL INFORMATION:
; APPLICANT: Biogen Idec Ma Inc.
; APPLICANT: Bailly, Veronique
; APPLICANT: Bonventre, Joseph
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: Molecules and Methods for Inhibiting
; FILE REFERENCE: A124 US
; CURRENT APPLICATION NUMBER: US/10/718,321
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/295449
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/295907
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US02/17402
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-718-321-6

Query Match 100.0%; Score 225; DB 17; Length 81;

Best Local Similarity 100.0%; Pred. No. 1e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLYSVTTGNDVTWSSDGLWNNQTQLEHSLLTANTTKG 42
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Sequence 19, Appli
Sequence 8, Appli
Sequence 25, Appli
Sequence 25, Appli
Sequence 25, Appli
Sequence 21, Appli
Sequence 21, Appli
Sequence 23, Appli
Sequence 27, Appli
Sequence 27, Appli
Sequence 6, Appli
Sequence 32, Appli
Sequence 39, Appli
Sequence 50, Appli
Sequence 1, Appli
Sequence 288232,
Sequence 343835,
Sequence 13, Appli
Sequence 13, Appli
Sequence 3, Appli
Sequence 9518, Ap
Sequence 20059, A
Sequence 9519, Ap
Sequence 59054, A
Sequence 196644,
Sequence 127039,
Sequence 37036, A
Sequence 514, App
Sequence 21, Appli
Sequence 19944, A
Sequence 220078,
Sequence 1975, Ap

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Db      40  PLYSYTTDGNDDTVTSSDGLWNNNQTLFLEHSLLTANTTKG 81

RESULT 2
US-10-655-506-7
; Sequence 7, Application US/10655506
; Publication No. US20050089868A1
; GENERAL INFORMATION:
; APPLICANT: Michele Sanicola-Nadel
;           Joseph V. Bonventre
;           Catherine A. Hession
;           Takaharu Ichimura
;           Henry Wei
;           Richard L. Cate
; TITLE OF INVENTION: MODULATORS OF TISSUE REGENERATION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/655,506
; FILING DATE: 04-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/197,970
; FILING DATE: 23-Nov-1998
; APPLICATION NUMBER: US 60/018,228
; FILING DATE: 24-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Levine, Leslie M.
; REGISTRATION NUMBER: 35,245
; REFERENCE/DOCKET NUMBER: A010 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 679-2810
; TELEFAX: (617) 679-2838
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 334 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-10-655-506-7

Query Match      100.0%; Score 225; DB 17; Length 334;
Best Local Similarity 100.0%; Pred. No. 5.6e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  PLYSYTTDGNDDTVTSSDGLWNNNQTLFLEHSLLTANTTKG 42
Db      249  PLYSYTTDGNDDTVTSSDGLWNNNQTLFLEHSLLTANTTKG 290

RESULT 3
US-10-718-321-7
; Sequence 7, Application US/10718321
; Publication No. US20050112117A1
; GENERAL INFORMATION:
; APPLICANT: Biogen Idec Ma Inc.
; APPLICANT: Bailly, Veronique
; APPLICANT: Bonventre, Joseph
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: Molecules and Methods for Inhibiting
; TITLE OF INVENTION: Shedding of KIM-1
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; FILE REFERENCE: A124 US
; CURRENT APPLICATION NUMBER: US/10/718,321
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/295449
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/295907
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US02/17402
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-718-321-7

Query Match      100.0%; Score 225; DB 17; Length 334;
Best Local Similarity 100.0%; Pred. No. 5.6e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  PLYSYTTDGNDDTVTSSDGLWNNNQTLFLEHSLLTANTTKG 42
Db      249  PLYSYTTDGNDDTVTSSDGLWNNNQTLFLEHSLLTANTTKG 290

RESULT 4
US-10-391-939A-2
; Sequence 2, Application US/10391939A
; Publication No. US20050014687A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W.;
; APPLICANT: Giot, Loic;
; APPLICANT: Guo, Xiaojia Sasha;
; APPLICANT: Lepley, Denise M.;
; APPLICANT: Mesri, Mehdi;
; APPLICANT: Ooi, Chean Eng;
; APPLICANT: Rastelli, Luca;
; APPLICANT: Rieger, Daniel K.;
; APPLICANT: Smithson, Glennda;
; APPLICANT: Starling, Gary;
; APPLICANT: Tse, Kam-Fai
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-048
; CURRENT APPLICATION NUMBER: US/10/391,939A
; CURRENT FILING DATE: 2003-03-19
; PRIOR APPLICATION NUMBER: 60/365,491
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/410,618
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 2
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-391-939A-2

Query Match      100.0%; Score 225; DB 17; Length 339;
Best Local Similarity 100.0%; Pred. No. 5.7e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  PLYSYTTDGNDDTVTSSDGLWNNNQTLFLEHSLLTANTTKG 42
Db      229  PLYSYTTDGNDDTVTSSDGLWNNNQTLFLEHSLLTANTTKG 270

RESULT 5
US-10-391-939A-28
; Sequence 28, Application US/10391939A
; Publication No. US20050014687A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W.;
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; APPLICANT: Giot, Loic ;
; APPLICANT: Guo, Xiaojia Sasha;
; APPLICANT: Lepley, Denise M.;
; APPLICANT: Mesri, Mehdi ;
; APPLICANT: Ooi, Chean Eng;
; APPLICANT: Rastelli, Luca ;
; APPLICANT: Rieger, Daniel K.;
; APPLICANT: Smithson, Glennda ;
; APPLICANT: Starling, Gary ;
; APPLICANT: Tse, Kam-Fai
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-048
; CURRENT APPLICATION NUMBER: US/10/391,939A
; CURRENT FILING DATE: 2003-03-19
; PRIOR APPLICATION NUMBER: 60/365,491
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/410,618
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 28
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-391-939A-28

Query Match      100.0%; Score 225; DB 17; Length 339;
Best Local Similarity 100.0%; Pred. No. 5.7e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLYSYTTDGNVTVTSSDGLWNNNTQLFLEHSLLTANTTKG 42
Db 229 PLYSYTTDGNVTVTSSDGLWNNNTQLFLEHSLLTANTTKG 270

RESULT 6
US-10-188-012-17
; Sequence 17, Application US/10188012
; Publication No. US20030124114A1
; GENERAL INFORMATION:
; APPLICANT: McIntire, Jennifer Jones
; APPLICANT: Umetsu, Dale T.
; APPLICANT: Dekruyff, Rosemarie
; APPLICANT: Kuchroo, Vijay
; APPLICANT: Freeman, Gordon J.
; TITLE OF INVENTION: T Cell Regulatory Genes and Methods of
; FILE REFERENCE: STAN-235
; CURRENT APPLICATION NUMBER: US/10/188,012
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/302,344
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 359
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(360)
; OTHER INFORMATION: TIM-1 allele 1
US-10-188-012-17

Query Match      100.0%; Score 225; DB 14; Length 359;
Best Local Similarity 100.0%; Pred. No. 6.2e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLYSYTTDGNVTVTSSDGLWNNNTQLFLEHSLLTANTTKG 42
Db 249 PLYSYTTDGNVTVTSSDGLWNNNTQLFLEHSLLTANTTKG 290

RESULT 7
US-10-188-012-19
; Sequence 19, Application US/10188012
; Publication No. US20030124114A1
; GENERAL INFORMATION:
; APPLICANT: McIntire, Jennifer Jones
; APPLICANT: Umetsu, Dale T.
; APPLICANT: Dekruyff, Rosemarie
; APPLICANT: Kuchroo, Vijay
; APPLICANT: Freeman, Gordon J.
; TITLE OF INVENTION: T Cell Regulatory Genes and Methods of
; FILE REFERENCE: STAN-235
; CURRENT APPLICATION NUMBER: US/10/188,012
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/302,344
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 359
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(359)
; OTHER INFORMATION: TIM-1, allele 2
US-10-188-012-19

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Best Local Similarity 100.0%; Pred. No. 6.2e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 249 PLYSYTTDGNVTVTSSDGLWNNNTQLFLEHSLLTANTTKG 290

RESULT 8
US-10-295-027-302
; Sequence 302, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/563,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
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; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 302
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-302

Query Match
Best Local Similarity 100.0%; Score 225; DB 15; Length 359;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLYSYTIDGNDVTVTSSDGLWNNNTQLFLEHSLLTANTTKG 42
|
Db 249 PLYSYTIDGNDVTVTSSDGLWNNNTQLFLEHSLLTANTTKG 290
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RESULT 9
US-10-188-832-64
; Sequence 64, Application US/10188832
; Publication No. US20040076955A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Natasha
; APPLICANT: Bos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-0023300S
; CURRENT APPLICATION NUMBER: US/10/188,832
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-832-64

Query Match
Best Local Similarity 100.0%; Score 225; DB 15; Length 359;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLYSYTIDGNDVTVTSSDGLWNNNTQLFLEHSLLTANTTKG 42
|
Db 249 PLYSYTIDGNDVTVTSSDGLWNNNTQLFLEHSLLTANTTKG 290
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RESULT 10
US-10-391-939A-4
; Sequence 4, Application US/10391939A
; Publication No. US20050014687A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W.;
; APPLICANT: Giot, Loic ;
; APPLICANT: Guo, Xiaojia Sasha;
; APPLICANT: Lepley, Denise M.;
```

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; APPLICANT: Mesri, Mehdi ;
; APPLICANT: Ooi, Chean Eng;
; APPLICANT: Rastelli, Luca ;
; APPLICANT: Rieger, Daniel K.;
; APPLICANT: Smithson, Glenda ;
; APPLICANT: Starling, Gary ;
; APPLICANT: Tse, Kam-Fai
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-048
; CURRENT APPLICATION NUMBER: US/10/391,939A
; CURRENT FILING DATE: 2003-03-19
; PRIOR APPLICATION NUMBER: 60/365,491
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/410,618
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 4
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-391-939A-4

Query Match
Best Local Similarity 100.0%; Score 225; DB 17; Length 359;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLYSYTIDGNDVTVTSSDGLWNNNTQLFLEHSLLTANTTKG 42
|
Db 249 PLYSYTIDGNDVTVTSSDGLWNNNTQLFLEHSLLTANTTKG 290
|

RESULT 11
US-10-663-497-17
; Sequence 17, Application US/10663497
; Publication No. US20050095593A1
; GENERAL INFORMATION:
; APPLICANT: Dale Umetsu
; APPLICANT: Rosemarie DeKruyff
; APPLICANT: Jennifer McIntire
; APPLICANT: Gordon Freeman
; TITLE OF INVENTION: T CELL REGULATORY GENES ASSOCIATED WITH
; TITLE OF INVENTION: IMMUNE DISEASE
; FILE REFERENCE: STAN-235CIP
; CURRENT APPLICATION NUMBER: US/10/663,497
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/302,344
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 10/188,012
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 359
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(360)
; OTHER INFORMATION: TIM-1 allele 1
US-10-663-497-17

Query Match
Best Local Similarity 100.0%; Score 225; DB 17; Length 359;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLYSYTIDGNDVTVTSSDGLWNNNTQLFLEHSLLTANTTKG 42
|
Db 249 PLYSYTIDGNDVTVTSSDGLWNNNTQLFLEHSLLTANTTKG 290
|

RESULT 12
US-10-663-497-19
```

; Sequence 19, Application US/10563497
; Publication No. US20050095593A1
; GENERAL INFORMATION:
; APPLICANT: Dale Umetsu
; APPLICANT: Rosemarie Dekruyff
; APPLICANT: Jennifer McIntire
; APPLICANT: Gordon Freeman
; TITLE OF INVENTION: T CELL REGULATORY GENES ASSOCIATED WITH
; TITLE OF INVENTION: IMMUNE DISEASE
; FILE REFERENCE: STAN-235CIP
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US/10/663,497
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/302,344
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 10/188,012
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 359
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(359)
; OTHER INFORMATION: TIM-1, allele 2
US-10-663-497-19

Query Match 100.0%; Score 225; DB 17; Length 359;
Best Local Similarity 100.0%; Pred. No. 6.2e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PLYSYTTCGNDVTSSDGLWNNQTLFLEHSLLTANTTKG 42
DB 249 PLYSYTTCGNDVTSSDGLWNNQTLFLEHSLLTANTTKG 290

RESULT 13
US-10-718-321-8
; Sequence 8, Application US/10718321
; Publication No. US2005011217A1
; GENERAL INFORMATION:
; APPLICANT: Biogen Idec Ma Inc.
; APPLICANT: Bailly, Veronique
; APPLICANT: Bonventre, Joseph
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: Molecules and Methods for Inhibiting
; TITLE OF INVENTION: Shedding of KIM-1
; FILE REFERENCE: A124 US
; CURRENT APPLICATION NUMBER: US/10/718,321
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/295449
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/295907
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US02/17402
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-718-321-8

Query Match 100.0%; Score 225; DB 17; Length 359;
Best Local Similarity 100.0%; Pred. No. 6.2e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PLYSYTTCGNDVTSSDGLWNNQTLFLEHSLLTANTTKG 42
DB 249 PLYSYTTCGNDVTSSDGLWNNQTLFLEHSLLTANTTKG 290

RESULT 14
US-10-847-918-25
; Sequence 25, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-847-918-25

Query Match 100.0%; Score 225; DB 17; Length 359;
Best Local Similarity 100.0%; Pred. No. 6.2e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PLYSYTTCGNDVTSSDGLWNNQTLFLEHSLLTANTTKG 42
DB 249 PLYSYTTCGNDVTSSDGLWNNQTLFLEHSLLTANTTKG 290

RESULT 15
US-10-188-012-25
; Sequence 25, Application US/10188012
; Publication No. US20030124114A1
; GENERAL INFORMATION:
; APPLICANT: McIntire, Jennifer Jones
; APPLICANT: Umetsu, Dale T.
; APPLICANT: Dekruyff, Rosemarie
; APPLICANT: Kuchroo, Vijay
; APPLICANT: Freeman, Gordon J.
; TITLE OF INVENTION: T Cell Regulatory Genes and Methods of
; FILE REFERENCE: STAN-235
; CURRENT APPLICATION NUMBER: US/10/188,012
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/302,344
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 364
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(364)
; OTHER INFORMATION: TIM-1 allele 5
US-10-188-012-25

Query Match 100.0%; Score 225; DB 14; Length 364;
Best Local Similarity 100.0%; Pred. No. 6.3e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PLYSYTTCGNDVTSSDGLWNNQTLFLEHSLLTANTTKG 42
DB 254 PLYSYTTCGNDVTSSDGLWNNQTLFLEHSLLTANTTKG 295

Search completed: June 29, 2005, 09:33:00

Job time : 26.3222 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 08:57:16 ; Search time 32.4637 Seconds
(without alignments)
1277.688 Million cell updates/sec

Title: US-10-718-321-6
Perfect score: 432
Sequence: 1 MFLPRQNHPEVATSSSPQ.....NNQTQLFLEHSLLTANTTKG 81

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03: *
1: uniprot_prot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	432	100.0	359	2	Q43656
2	432	100.0	364	2	Q96D42
3	348	80.6	451	2	Q95144
4	348	80.6	460	2	O18984
5	335	77.5	469	2	Q7J348
6	335	77.5	473	2	Q7J347
7	335	77.5	474	2	O46597
8	335	77.5	478	2	O46598
9	89	20.6	307	2	O54947
10	86	19.9	315	2	Q7PMD5
11	86	19.9	315	2	Q7PMD5
12	83	19.2	642	2	Q75UG6
13	82.5	19.1	684	2	Q8S824
14	79.5	18.4	965	2	Q22286
15	79	18.3	681	2	Q9PFW5
16	77	17.8	440	2	O9A716
17	77	17.8	1139	2	Q6NTK5
18	76.5	17.7	282	2	Q8VIM1
19	76.5	17.7	282	2	Q7TPU2
20	76	17.6	875	2	Q9H706
21	76	17.6	1006	2	Q62901
22	75.5	17.5	224	2	Q9CR77
23	75.5	17.5	303	2	Q9D116
24	75.5	17.5	303	2	Q8R3W0
25	75.5	17.5	319	2	Q8BP27
26	75.5	17.5	319	2	Q9D0D7
27	75.5	17.5	319	2	Q9D4W4
28	75.5	17.5	1146	2	Q8X0L3
29	75	17.4	670	2	Q6BVR2
30	75	17.4	777	2	Q9BSF5
31	75	17.4	877	2	Q8ND03

32	74.5	17.2	298	2	Q9U5E7
33	74.5	17.2	1015	2	Q8GAG0
34	73.5	17.0	823	2	Q75IH8
35	73.5	17.0	2819	2	Q8BEN8
36	73	16.9	579	2	Q6P50
37	73	16.9	709	2	Q86A80
38	73	16.9	982	2	Q6CSV5
39	73	16.9	1423	2	Q7YS39
40	72.5	16.8	338	2	Q9SQQ6
41	72.5	16.8	634	2	Q7RJ33
42	72.5	16.8	760	1	ABB2 MOUSE
43	72.5	16.8	837	2	Q7QF61
44	72.5	16.8	888	2	Q6PB73
45	72.5	16.8	1082	2	Q6PDP0

ALIGNMENTS

RESULT 1
O43656 PRELIMINARY; PRT; 359 AA.
AC O43656;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT - 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hepatitis A virus cellular receptor 1.
GN Name=HAVCr-1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98325180; PubMed=9658108;
RA Feigelsstock D., Thompson P., Mattoo P., Zhang Y., Kaplan G.G.;
RT "The human homolog of HAVcr-1 codes for a hepatitis A virus cellular receptor.";
RL J. Virol. 72:6621-6628(1998).
DR ENBL; AF043724; AAC39862.1; -.
DR GO; GO:0004872; Fireceptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG_1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 359 AA; 38704 MW; C207FEC562DC62CA CRC64;

Query Match 100.0%; Score 432; DB 2; Length 359;
Best Local Similarity 100.0%; Pred.No. 2.9e-33;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MFLPRQNHPEVATSSSPQAEHTPTTLQCAIRREPTSSPLSYTTDGDNDVTSSDGLW 60
Db	210	MFLPRQNHPEVATSSSPQAEHTPTTLQCAIRREPTSSPLSYTTDGDNDVTSSDGLW 269
QY	61	NNQTQLFLEHSLLTANTTKG 81
Db	270	NNQTQLFLEHSLLTANTTKG 290

RESULT 2
Q96D42 PRELIMINARY; PRT; 364 AA.
AC Q96D42;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE HAVCr1 protein.
GN Name=HAVCr1;


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QY 62 NNQTLFLEHSLLTANTTKG 81
DB 360 NNQTLSPHSPQMVNTTEG 379

RESULT 5
Q7JJ48
ID AC Q7JJ48 PRELIMINARY; PRT; 469 AA.
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE Hepatitis A virus cellular receptor 1 short form.
GN Name=HAVcr-1;
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98285791; PubMed=9621093;
RA Feigelsstock D., Thompson P., Mattoo P., Kaplan G.G.;
RT "Polymorphisms of the hepatitis A virus cellular receptor 1 in African
RT green monkey kidney cells result in antigenic variants that do not
RT react with protective monoclonal antibody 190/4.";
RL J. Virol. 72:6218-6222(1998).
DR EMBL; AF043446; AAC39771.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 469 AA; 50561 MW; 27E386F47948F528 CRC64;

Query Match 77.5%; Score 335; DB 2; Length 469;
Best Local Similarity 80.0%; Pred. No. 7.9e-24;
Matches 64; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 2 PLPRNHPEVATSPSPQPAETHPTTLOGAIRREPTSSPLSYTTDGNNTVTSSDGLWN 61
DB 309 PLPMQDHEPVATSPSSAQPAETHPTVLLGATRTQPTSSPLSYTTDGS DTVTSSDGLWN 368

QY 62 NNQTLFLEHSLLTANTTKG 81
DB 369 NNQTLSPHSPQMVNTTEG 388

RESULT 6
Q7JJ47
ID AC Q7JJ47 PRELIMINARY; PRT; 473 AA.
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE Hepatitis A virus cellular receptor 1 short form.
GN Name=HAVcr-1;
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98285791; PubMed=9621093;
RA Feigelsstock D., Thompson P., Mattoo P., Kaplan G.G.;
RT "Polymorphisms of the hepatitis A virus cellular receptor 1 in African
RT green monkey kidney cells result in antigenic variants that do not
RT react with protective monoclonal antibody 190/4.";
RL J. Virol. 72:6218-6222(1998).
DR EMBL; AF043447; AAC39772.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 473 AA; 51088 MW; 472DF987CA220524 CRC64;

Query Match 77.5%; Score 335; DB 2; Length 474;
Best Local Similarity 80.0%; Pred. No. 8e-24;
Matches 64; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 2 PLPRNHPEVATSPSPQPAETHPTTLOGAIRREPTSSPLSYTTDGNNTVTSSDGLWN 61
DB 314 PLPMQDHEPVATSPSSAQPAETHPTVLLGATRTQPTSSPLSYTTDGS DTVTSSDGLWN 373

QY 62 NNQTLFLEHSLLTANTTKG 81
DB 374 NNQTLSPHSPQMVNTTEG 393

RESULT 8
O46598

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RL J. Virol. 72:6218-6222(1998).
DR EMBL; AF043448; AAC39773.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 473 AA; 50973 MW; CD15EP5EE79C8013 CRC64;

Query Match 77.5%; Score 335; DB 2; Length 473;
Best Local Similarity 80.0%; Pred. No. 8e-24;
Matches 64; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 2 PLPRNHPEVATSPSPQPAETHPTTLOGAIRREPTSSPLSYTTDGNNTVTSSDGLWN 61
DB 313 PLPMQDHEPVATSPSSAQPAETHPTVLLGATRTQPTSSPLSYTTDGS DTVTSSDGLWN 372

QY 62 NNQTLFLEHSLLTANTTKG 81
DB 373 NNQTLSPHSPQMVNTTEG 392

RESULT 7
O46597
ID AC O46597 PRELIMINARY; PRT; 474 AA.
DT 01-JUN-1998 (TREMELrel. 06, Created)
DT 01-JUN-1998 (TREMELrel. 06, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Hepatitis A virus cellular receptor 1 long form.
GN Name=HAVcr-1;
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98285791; PubMed=9621093;
RA Feigelsstock D., Thompson P., Mattoo P., Kaplan G.G.;
RT "Polymorphisms of the hepatitis A virus cellular receptor 1 in African
RT green monkey kidney cells result in antigenic variants that do not
RT react with protective monoclonal antibody 190/4.";
RL J. Virol. 72:6218-6222(1998).
DR EMBL; AF043447; AAC39772.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 474 AA; 51088 MW; 472DF987CA220524 CRC64;

Query Match 77.5%; Score 335; DB 2; Length 474;
Best Local Similarity 80.0%; Pred. No. 8e-24;
Matches 64; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 2 PLPRNHPEVATSPSPQPAETHPTTLOGAIRREPTSSPLSYTTDGNNTVTSSDGLWN 61
DB 314 PLPMQDHEPVATSPSSAQPAETHPTVLLGATRTQPTSSPLSYTTDGS DTVTSSDGLWN 373

QY 62 NNQTLFLEHSLLTANTTKG 81
DB 374 NNQTLSPHSPQMVNTTEG 393

RESULT 8
O46598

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ID O46598 PRELIMINARY; PRT; 478 AA.
AC O46598;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hepatitis A virus cellular receptor 1 long form.
GN Name=HAVcr-1;
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98285791; PubMed=9621093;
RA Feigelsstock D., Thompson P., Matteo P., Kaplan G.G.;
RT "Polymorphisms of the hepatitis A virus cellular receptor 1 in African
RT green monkey kidney cells result in antigenic variants that do not
RT react with protective monoclonal antibody 190/4.";
RL J. Virol. 72:6218-6222(1998).
DR EMBL; AF043449; AAC39774.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR Receptor.
SQ SEQUENCE 478 AA; 51501 MW; 3A919655C752FF60 CRC64;

Query Match 77.5%; Score 335; DB 2; Length 478;
Best Local Similarity 80.0%; Pred. No. 8.1e-24;
Matches 64; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 2 PLPRONHEPVATSPSPQPAETHPTTLOGAIRREPTSSPLYSTYTDGNDVTSSDGLWN 61
Db 318 PLPMQDHEPVATSPSSAQPAETHVLLGATRTQTSSPLSYSTYTDGSDVTSSDGLWN 377

QY 62 NNQTQLFLEHSLTLTANTYKG 81
Db 378 NNQTQLSPHSPQMVNTTTEG 397

RESULT 9
OS4947 PRELIMINARY; PRT; 307 AA.
AC O54947;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Kidney injury molecule-1 (KIM-1 protein).
GN Name=KIM-1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley; TISSUE=Kidney;
RX MEDLINE=98129827; PubMed=9461608; DOI=10.1074/jbc.273.7.4135;
RA Ichimura T., Bonventre J.V., Bailly V., Wei H., Hession C.A.,
RA Cate R.B., Sanicola M.;
RT "Kidney injury molecule-1 (KIM-1), a putative epithelial cell adhesion
RT molecule containing a novel immunoglobulin domain, is up-regulated in
RT renal cells after injury.";
RL J. Biol. Chem. 273:4135-4142(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshituki S., Carninci P., Prange C.,
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshituki S., Carninci P., Prange C.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF035963; AAC3546.1; -.
DR EMBL; BC061820; AAH61820.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR Receptor.
SQ SEQUENCE 307 AA; 33963 MW; 736D1DD1F1549760 CRC64;

Query Match 20.6%; Score 89; DB 2; Length 307;
Best Local Similarity 34.1%; Pred. No. 1.7;
Matches 31; Conservative 9; Mismatches 27; Indels 24; Gaps 6;

QY 5 ROMEHPVAT--SPSPQPAET-----HPTTLOGAIRREPTSSPLYSTYTDGND 50
Db 155 RSTHYPTSTRVSTSTPTPEQTQTHKPEITTFYAHETT-----AEVTETPSYT-PADWNG 207

QY 51 TVTSSDGLWNNTQFLFLEHSLTLTANTYKG 81
Db 208 TVT-SSEAWNNHTVIRLRKP--QRNPTKG 235

RESULT 10
QY7L9D0 PRELIMINARY; PRT; 153 AA.
AC Q7L9D0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein FLJ22174 (Hypothetical protein FLJ21380).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
RA Suzuki Y., Ohtsuka M., Nishi T., Shibahara T., Tanaka T.,
RA Nakamura Y., Isono T., Sugano S.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBSJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshituki S., Carninci P., Prange C.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF035963; AAC3546.1; -.
DR EMBL; BC061820; AAH61820.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR Receptor.
SQ SEQUENCE 307 AA; 33963 MW; 736D1DD1F1549760 CRC64;

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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Boeak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettaman M., Madan A.C., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young J.W., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.B.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
 RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR ENBL; AK025827; BAB15250.1; -;
 DR ENBL; BC022217; AAH2217.1; -;
 DR ENBL; AK025033; BAB15054.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 153 AA; 16678 MW; 11CA3A27EDCE711F CRC64;

Query Match 20.4%; Score 88; DB 2; Length 153;
 Best Local Similarity 41.7%; Pred. No. 0.91;
 Matches 20; Conservative 6; Mismatches 10; Indels 12; Gaps 2;
 QY 3 LPRQNHVPATSSSPQAPAE-----THPTTL-----QCAIRREPTS 38
 DB 46 LPBQHPVGTAPGNVPSPQGGRTHTPSLIRIWARRAQOGRLLRLPTS 93

RESULT 11
 Q7PMD5 ID Q7PMD5 PRELIMINARY; PRT; 3150 AA.
 AC Q7PMD5;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE ENSANGP0000004655 (Fragment).
 GN Name=ENSANGG00000003651;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR ENBL; AAAA01008980; EAA13969.2; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
 DR InterPro; IPR006770; OGF_recept.
 DR Pfam; PF04680; OGF_III; 80.
 FT NON_TER 1 3150
 FT NON_TER 3150 3150
 SQ SEQUENCE 3150 AA; 322879 MW; 3C7B3D441C8C839 CRC64;

Query Match 19.9%; Score 86; DB 2; Length 3150;
 Best Local Similarity 34.4%; Pred. No. 57;
 QY 2 PLPRQNHVPATSSSPQAPAEHTTTTQGAIRREPTSSSPLYSYTTDGNVTSSDGLWN 61
 DB 1293 PESTPTTGIRTSPTPTSTESDITMSSASTPEPTTPDTRTTPRTSTESTDITMS 1352
 QY 62 NNOT 65
 DB 1353 SAST 1356

Matches 22; Conservative 9; Mismatches 33; Indels 0; Gaps 0;
 QY 2 PLPRQNHVPATSSSPQAPAEHTTTTQGAIRREPTSSSPLYSYTTDGNVTSSDGLWN 61
 DB 1293 PESTPTTGIRTSPTPTSTESDITMSSASTPEPTTPDTRTTPRTSTESTDITMS 1352
 QY 62 NNOT 65
 DB 1353 SAST 1356

RESULT 12
 Q75JG6 ID Q75JG6 PRELIMINARY; PRT; 642 AA.
 AC Q75JG6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Similar to Leishmania major. Ppg3.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX4;
 RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
 RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
 RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
 RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
 RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum";
 RL Nature 418:79-85(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX4;
 RA Baumgart C.;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 DR ENBL; AC116979; AAS38767.1; -;
 SQ SEQUENCE 642 AA; 66631 MW; C4837BCCEFA4962A CRC64;

Query Match 19.2%; Score 83; DB 2; Length 642;
 Best Local Similarity 29.5%; Pred. No. 16;
 Matches 26; Conservative 16; Mismatches 32; Indels 14; Gaps 4;
 QY 2 PLPRQNHVPATSSSPQAPAEHTTTTQGAIRREPT-----SSPLYSYTTDGNVTES 55
 DB 461 PPTNSSSTPTTNSSTPTP--TNSSTPTTNSDPSASSFSSSFSNSTSSNSTSPS 518
 QY 56 SDGLMNNNOTQLF-----LEHSLLTANTT 79
 DB 519 SSSL--NNSTSFNSTSLNSTSSNST 544

RESULT 13
 Q8SSZ4 ID Q8SSZ4 PRELIMINARY; PRT; 684 AA.
 AC Q8SSZ4;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX4;
 RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
 RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
 RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
 RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
 RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum";
 RL Nature 418:79-85(2002).
 RN [2]


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DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR PRINTS; PR01218; PSTLEXTENSIN.
DR PRODOM; PD000001; Prot kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 681 AA; 72389 MW; F64DAA1E470E73F9 CRC64;

Query Match      18.3%; Score 79; DB 2; Length 681;
Best Local Similarity 29.8%; Pred. No. 41;
Matches 17; Conservative 11; Mismatches 29; Indels 0; Gaps 0;

Qy      2 PLPRQNHVPATSPSPQPAETHPTLQGAIRREPTSSPLYSYTTGNDVTWESSDG 58
Db      173 PPPATSGASPPSSNPTDPSTLAPPPTPLPVVPREKPIAKPTGPASNNGNNTLPSSSPG 229

Search completed: June 29, 2005, 09:01:42
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